



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 153564

**TO: Minh-Tam Davis**  
**Location: REM/3A24/3C18**  
**Art Unit: 1642**  
**Friday, May 20, 2005**

**Case Serial Number: 09/976858**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**Remsen 1-A-62**  
**Phone: 571-272-2524**

**maryjane.ruhl@uspto.gov**

### Search Notes

Examiner Davis,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524



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From: Chan, Christina  
Sent: Monday, May 16, 2005 4:39 PM  
To: Davis, Minh-Tam; STIC-Biotech/ChemLib  
Subject: RE: Rush search request for 09/976858

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

From: Davis, Minh-Tam  
Sent: Monday, May 16, 2005 3:53 PM  
To: Chan, Christina  
Subject: Rush search request for 09/976858

Please search in commercial database, issued patent files, PGPUB and interference:

- 1) SEQ ID NO:41
- 2) oligomer search for SEQ ID NO:41, with size limitation for the sequences in the database less than 500 nucleotides.

Please have the search results in both paper and disk.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18  
272-0830

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 16:18:52 ; Search time 1981 Seconds  
(without alignments)  
11887.295 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcccgtgtaccagga.....ttttcagagacagcactgtga 3978

Scoring table: OLIGO\_NUC

Gapop\_60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6273088

Minimum DB seq length: 0

Maximum DB seq length: 500

Post-processing: Listing first 45 summaries

Database: N\_Geneseq\_16Dec04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	366	9.2	486	2 AAT94053	Aat94053 Partial h
C 2	336	8.4	424	5 ABV40627	Abv40627 Human pro
C 3	308	7.7	407	5 ABV40332	Abv40332 Human pro
4	283	7.1	442	5 ABV24239	Abv24239 Human pro
5	252	6.3	425	5 ABV41910	Abv41910 Human pro
6	216	5.4	291	4 AAH93897	Aah93897 P510S-C c
7	216	5.4	291	4 AAS64133	Aas64133 Human CDN
8	216	5.4	291	5 ACA59941	Aca59941 Prostate
9	216	5.4	291	6 ABV95504	Abv95504 P510S-C c
10	216	5.4	291	8 ACC95668	Acc95668 Prostate
11	216	5.4	291	10 ADB14273	Adb14273 Human pro
12	216	5.4	291	10 ADG26689	Adg26689 Human pro
13	211	5.3	439	2 AAX40493	Aax40493 Human sec
14	210	5.3	391	5 ABV41670	Abv41670 Human pro
15	208	5.2	444	5 ABV32629	Abv32629 Human pro
16	208	5.2	482	5 ABV11484	Abv11484 Human pro
17	196	4.9	456	5 ABV21425	Abv21425 Human pro
18	196	4.9	456	5 ABV27243	Abv27243 Human pro
C 19	176	4.4	345	5 ABV10192	Abv10192 Human pro
C 20	176	4.4	412	5 ABV31363	Abv31363 Human pro

C	21	145	3.6	273	5	ABV38375	Abv38375 Human pro
	22	142	3.6	329	5	ABV32745	Abv32745 Human pro
	23	142	3.6	416	5	ABV11600	Abv11600 Human pro
C	24	141	3.5	409	5	ABV11417	Abv11417 Human pro
C	25	141	3.5	433	5	ABV41487	Abv41487 Human pro
C	26	141	3.5	433	5	ABV32562	Abv32562 Human pro
	27	138	3.5	469	5	ABV27424	Abv27424 Human pro
	28	138	3.5	469	5	ABV21605	Abv21605 Human pro
	29	138	3.5	469	5	ABV20845	Abv20845 Human pro
	30	137	3.4	350	5	ABV13007	Abv13007 Human pro
	31	137	3.4	425	5	ABV03838	Abv03838 Human pro
C	32	136	3.4	462	5	ABV02188	Abv02188 Human pro
C	33	136	3.4	484	5	ABV11357	Abv11357 Human pro
C	34	133	3.3	372	5	ABV02248	Abv02248 Human pro
	35	132	3.3	403	5	ABV11840	Abv11840 Human pro
	36	132	3.3	422	5	ABV32985	Abv32985 Human pro
	37	127	3.2	391	5	ABV06629	Abv06629 Human pro
C	38	125	3.1	439	5	ABV36508	Abv36508 Human pro
	39	114	2.9	281	5	ABV36609	Abv36609 Human pro
	40	111	2.8	432	5	ABV37059	Abv37059 Human pro
	41	110	2.8	339	5	ABV36578	Abv36578 Human pro
	42	105	2.6	220	5	ABV06661	Abv06661 Human pro
	43	98	2.5	377	12	ADH10618	Adh10618 Human Can
	44	93	2.3	387	5	ABV02315	Abv02315 Human pro
C	45	91	2.3	363	5	ABV06557	Abv06557 Human pro

#### ALIGNMENTS

##### RESULT 1

AAT94053

ID AAT94053 standard; cDNA; 486 BP.

XX AAT94053;

XX 25-MAR-2003 (revised)

DT 01-APR-1998 (first entry)

XX Partial human multidrug resistance-associated protein 4 (hMRP4) cDNA.

DE Partial human multidrug resistance-associated protein 4 (hMRP4) cDNA.

XX Canicular multispecific organic anion transporter protein;

KW cMOAT protein; ATP-binding cassette transporter family; ABC transporter;

KW hepatobiliary excretion; multidrug resistance-associated protein; MRP4;

KW cMOAT protein activity; multidrug resistance-related protein; MDR-1;

KW Dubin-Johnson disease; Rotor disease; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO9731111-A2.

PN 28-AUG-1997.

XX 21-FEB-1997; 97WO-NL000079.

XX 22-FEB-1996; 96EP-00200460.

XX (INTR-) INTROGENE BV.

PA (MEDI-) ACAD MEDISCH CENT AMSTERDAM.

PA (HETN-) HET NEDERLANDS KANKER INST.

XX Oude Elferink RPJ, Paulusma CC, Bosma PJ, Borst P, Evers R;

PI Kool M;

XX WPI; 1997-435163/40.

DR DNA encoding human and rat canalicular multispecific organic anion

XX transporter proteins - useful for diagnosis and treatment of Dubin-

PT Johnson disease and Rotor disease.

XX Disclosure; Fig 18; 106pp; English.

PS The present cDNA sequence encodes a partial human multidrug resistance-

XX

CC

CC associated protein 4 (MRP4). The MRP4 gene has been localised to  
 CC chromosome 13. The MRP4 protein is a member of the ATP-binding cassette  
 CC (ABC) transporter family of anorganic anion transporters. MRP4 is a 4  
 CC domain protein, with 2 ATP-binding domains, and 2 domains with  
 CC transmembrane regions. The protein is a homologue of MRP1, which is  
 CC involved in ATP-dependent transport of glutathione conjugates such as  
 CC dinitrophenyl glutathione. These substrates are also transported by a  
 CC canalicular multispecific organic anion transporter (cMOAT) protein. The  
 CC ATP dependent cMOAT transporter system mediates hepatobiliary excretion  
 CC in the liver. cMOAT may be a liver-specific homologue of multidrug  
 CC resistance-associated protein. The nucleic acids are used to provide  
 CC cells with cMOAT protein activity. cMOAT protein activity in cells can be  
 CC enhanced by increasing the level of glutathione, glucuronide and/or  
 CC sulphate. Antisense constructs, especially derived from another multidrug  
 CC resistance (MDR)-related protein, e.g. MDR-1, to the nucleic acids and  
 CC vectors can be used to decrease the level of cMOAT in a cell. The nucleic  
 CC acids and proteins can be used especially in diagnosis of Dubin-Johnson  
 CC disease, Rotor disease or another disease involving cMOAT. The cMOAT gene  
 CC may also be used as a selectable marker gene. (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 CC  
 XX

SQ Sequence 486 BP; 169 A; 84 C; 99 G; 113 T; 0 U; 21 Other;

Query Match 9.2%; Score 366; DB 2; Length 486;

Best Local Similarity 100.0%; Pred. No. 1.3e-171; Length 486;

Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3462 ACTTAAGAAACCAATGAAGATCTTCTGGTAAATGGATAGTGAATAGCAGATCAGG 3521

Db 1 ACTTAAGAAACCAATGAAGATCTTCTGGTAAATGGATAGTGAATAGCAGATCAGG 60

Qy 3522 ATCCAAATTTAGTTGGACAAACAACTGGTGTGCTTCCAGGGCAATTCAGGAA 3581

Db 61 ATCCAAATTTAGTTGGACAAACAACTGGTGTGCTTCCAGGGCAATTCAGGAA 120

Qy 3582 AAATCAGATATTGATTTGATGAAGCGACGCAAAATGTGGATCCAAAGAACTGATGATT 3641

Db 121 AAATCAGATATTGATTTGATGAAGCGACGCAAAATGTGGATCCAAAGAACTGATGATT 180

Qy 3642 AATACAAAAAATTCGGGAGAAATTTGCCACTGCACCGTGTAAACCAATTCACACAG 3701

Db 181 AATACAAAAAATTCGGGAGAAATTTGCCACTGCACCGTGTAAACCAATTCACACAG 240

Qy 3702 ATTGAACACCAATTTGACACGCAAGATATGTTTGTAGATTCAGGAGAACTGAAAGA 3761

Db 241 ATTGAACACCAATTTGACACGCAAGATATGTTTGTAGATTCAGGAGAACTGAAAGA 300

Qy 3762 ATATGATGAGCGGTATGTTTGTGCAAAATATAAGAGAGCGCTATTATTACAGATGGTGCA 3821

Db 301 ATATGATGAGCGGTATGTTTGTGCAAAATATAAGAGAGCGCTATTATTACAGATGGTGCA 360

Qy 3822 ACAACT 3827

Db 361 ACAACT 366

RESULT 2

ABV40627/c

ID ABV40627 standard; cDNA; 424 BP.

XX

AC ABV40627;

XX

DT 16-SEP-2002 (first entry)

XX

DE Human prostate expression marker cDNA 40618.

XX

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX

OS pharmacogenomic marker; gene; ss.

XX

PN Homo sapiens.

XX

WO200160860-A2.

XX

PD 23-AUG-2001.

XX

PF 20-FEB-2001; 2001WO-US005171.

XX

PR 17-FEB-2000; 2000US-0183319P.

PR 16-MAR-2000; 2000US-0189862P.

PR 25-MAY-2000; 2000US-0207454P.

PR 09-JUN-2000; 2000US-0211314P.

PR 18-JUL-2000; 2000US-0219007P.

PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PA

PI Schlegel R, Endege WO, Monahan JE;

XX

XX WPI; 2001-662795/76.

DR

XX

PT Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.

XX

PS Claim 1; Page 8189; 11750pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the

CC progression of prostate cancer in a patient; (c) assessing the efficacy

CC of a test compound to inhibit prostate cancer in a patient; (d) assessing

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)

CC determining whether prostate cancer has metastasized in a patient; (h)

CC assessing the aggressiveness or indolence of prostate cancer in a patient

CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX

SQ Sequence 424 BP; 116 A; 104 C; 94 G; 110 T; 0 U; 0 Other;

Query Match 8.4%; Score 336; DB 5; Length 424;

Best Local Similarity 100.0%; Pred. No. 1.3e-156;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 532 GCATTCGTCTTAGTAACATGGCCATGGGAAGAACACACAGGCCAGATAGTCAATCTG 591

Db 381 GCATTCGTCTTAGTAACATGGCCATGGGAAGAACACACAGGCCAGATAGTCAATCTG 322

Qy 592 CTGTCCAATGATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTTACACTTCTCTGTGGCA 651

Db 321 CTGTCCAATGATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTTACACTTCTCTGTGGCA 262

Qy 652 GGACCACTGCAGGGGATCGCAGTGCCTCTCTGCTGAGTAGGATAGTATCGTGC 711

Db 261 GGACCACTGCAGGGGATCGCAGTGCCTCTCTGCTGAGTAGGATAGTATCGTGC 202

Qy 712 CTGCTGGGATGGCAGTCTTAATCATTTCTCTGCTGCTTGCAGAGCTGTTTGGGAAGTTG 771

Db 201 CTGCTGGGATGGCAGTCTTAATCATTTCTCTGCTGCTTGCAGAGCTGTTTGGGAAGTTG 142

Qy 772 TTCTCATCTAGGAGTAAACCTGCAACTTTTACCGGATGCCAGATCAGACCATGAAT 831

Db 141 TTCTCATCTAGGAGTAAACCTGCAACTTTTACCGGATGCCAGATCAGACCATGAAT 82

Qy 832 GAAGTTTAACTGGTATAGGATTAATAAATGTAC 867

Db 81 GAAGTTTAACTGGTATAGGATTAATAAATGTAC 46

RESULT 3

ABV40332/c

ID ABV40332 standard; cDNA; 407 BP.

XX

AC ABV40332;

XX

DT 16-SEP-2002 (first entry)  
 XX Human prostate expression marker cDNA 40323.  
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 OS Homo sapiens.  
 XX WO200160860-A2.  
 XX 23-AUG-2001.  
 XX 20-FEB-2001; 2001WO-US005171.  
 XX 17-FEB-2000; 2000US-0183319P.  
 XX 16-MAR-2000; 2000US-0189862P.  
 XX 25-MAY-2000; 2000US-0207454P.  
 XX 09-JUN-2000; 2000US-0211314P.  
 XX 18-JUL-2000; 2000US-0219007P.  
 XX 13-DEC-2000; 2000US-0255281P.  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX Schlegel R, Endege WO, Monahan JE;  
 XX WPI; 2001-662795/76.  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer.  
 XX Claim 1; Page 8142; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 407 BP; 108 A; 96 C; 97 G; 106 T; 0 U; 0 Other;  
 Query Match 7.7%; Score 308; DB 5; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-142;  
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1955 GTACCTTCTCAGAGTCTTGGTTGGTCTCAACATCTTCTAGACCTCTTGAAGATG 2014  
 Db 374 GTACCTTCTCAGAGTCTTGGTTGGTCTCAACATCTTCTAGACCTCTTGAAGATG 315  
 Qy 2015 GTGCTCTGGAGCCAGATACAGAGATGTCCTAGTACACTATCAGAGGAGACCGTT 2074  
 Db 314 GTGCTCTGGAGCCAGATACAGAGATGTCCTAGTACACTATCAGAGGAGACCGTT 255  
 Qy 2075 CTGAAGGAAATGTTGGTTTTCAGGCTTAAGAATTACTTCAGAGCTGGTCTCACTGGA 2134  
 Db 254 CTGAAGGAAATGTTGGTTTTCAGGCTTAAGAATTACTTCAGAGCTGGTCTCACTGGA 195  
 Qy 2135 TTGCTTCATTTCTTATTTCTTAAACACTGAGCTCAGGTGCTTATGCTTCAAG 2194  
 Db 194 TTGCTTCATTTCTTATTTCTTAAACACTGAGCTCAGGTGCTTATGCTTCAAG 135  
 Qy 2195 ATTGGTGGCTTTTACTATGCGGCAACAAACAAAGTATGCTAAATGCTACTGTAATGGAG 2254  
 Db 134 ATTGGTGGCTTTTACTATGCGGCAACAAACAAAGTATGCTAAATGCTACTGTAATGGAG 75

Qy 2255 GAGGAAT 2262  
 Db 74 GAGGAAT 67  
 RESULT 4  
 ABV24239  
 ID ABV24239 standard; cDNA; 442 BP.  
 XX AC ABV24239;  
 XX 16-SEP-2002 (first entry)  
 XX Human prostate expression marker cDNA 24230.  
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX Homo sapiens.  
 XX WO200160860-A2.  
 XX 23-AUG-2001.  
 XX 20-FEB-2001; 2001WO-US005171.  
 XX 17-FEB-2000; 2000US-0183319P.  
 XX 16-MAR-2000; 2000US-0189862P.  
 XX 25-MAY-2000; 2000US-0207454P.  
 XX 09-JUN-2000; 2000US-0211314P.  
 XX 18-JUL-2000; 2000US-0219007P.  
 XX 13-DEC-2000; 2000US-0255281P.  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX Schlegel R, Endege WO, Monahan JE;  
 XX WPI; 2001-662795/76.  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer.  
 XX Claim 1; Page 4528; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 442 BP; 121 A; 91 C; 110 G; 120 T; 0 U; 0 Other;  
 Query Match 7.1%; Score 283; DB 5; Length 442;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-130;  
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 532 GCATTCGTCTTAGTAATGCCATGGGGAAGAACACACAGCCAGATAGTCAATCTG 591  
 Db 109 GCATTCGTCTTAGTAATGCCATGGGGAAGAACACACAGCCAGATAGTCAATCTG 168  
 Qy 592 CTGTCCAAATGATGAAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCA 651  
 Db 169 CTGTCCAAATGATGAAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCA 228  
 Qy 652 GGACCACTGCGGCGATCGCAGTGAATGCTTCTGATGGAGATAGGAATATCGTGC 711

Db 229 GGACCACTGGGGGATCGAGTGAATGCGCCCTACTCTGGATGGAGATAGGATATCGTGC 288  
Qy 712 CTGCTGGAGTGGCAGTCTTAATCATCTCTGCGCCCTTGGCAAGCTGTTTGGGAAGTTG 771  
Db 289 CTGCTGGAGTGGCAGTCTTAATCATCTCTGCGCCCTTGGCAAGCTGTTTGGGAAGTTG 348  
Qy 772 TTCTCATCACTGAGGAGTAAACTGCACTTTTACGGATGCCAGATCAGGACCATGAAT 831  
Db 349 TTCTCATCACTGAGGAGTAAACTGCACTTTTACGGATGCCAGATCAGGACCATGAAT 408  
Qy 832 GAAAGTTAATCTGGTATAGGATTAATAAATAATGT 865  
Db 409 GAAAGTTAATCTGGTATAGGATTAATAAATAATGT 442

## RESULT 5

ID ABV41910 standard; cDNA; 425 BP.

XX AC ABV41910;  
XX DT

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 41901.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX OS Homo sapiens.

XX PN WO200160860-A2.  
XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.  
XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.  
XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.  
XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.  
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;  
XX DR WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 8407-8408; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

SQ Sequence 425 BP; 108 A; 91 C; 102 G; 124 T; 0 U; 0 Other;  
Query Match 6.3%; Score 252; DB 5; Length 425;  
Best Local Similarity 100.0%; Pred. No. 1.2e-114;

Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 532 GCATTCGCTTTAGTAACATGGCCATGGGGAAGCAACACAGCCAGATAGTCAATCTG 591  
Db 174 GCATTCGCTTTAGTAACATGGCCATGGGGAAGCAACACAGCCAGATAGTCAATCTG 233  
Qy 592 CTGTCCAATGATGTGAACAAGTTTGTGATCAGTGACAGTGTCTTACACTTCTCTGTGGCA 651  
Db 234 CTGTCCAATGATGTGAACAAGTTTGTGATCAGTGACAGTGTCTTACACTTCTCTGTGGCA 293  
Qy 652 GGACCACTGAGGCGATCGCAGTGAATCTCTGATGGAGATAGGAATATCGTGC 711  
Db 294 GGACCACTGAGGCGATCGCAGTGAATCTCTGATGGAGATAGGAATATCGTGC 353  
Qy 712 CTGTCTGGGATGGCAGTCTTAATCATTTCTCTGCGCCCTTGCACAGCTGTTTGGGAAGTTG 771  
Db 354 CTGTCTGGGATGGCAGTCTTAATCATTTCTCTGCGCCCTTGCACAGCTGTTTGGGAAGTTG 413  
Qy 772 TTCTCATCACTG 783  
Db 414 TTCTCATCACTG 425

## RESULT 6

ID AAH93897 standard; cDNA; 291 BP.

XX AC AAH93897;  
XX DT

XX 04-OCT-2001 (first entry)

XX PS10S-C construct cDNA sequence.

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;  
KW cytostatic; gene therapy; metastasis; ss.  
XX OS Homo sapiens.

XX PN WO200151633-A2.  
XX PD 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US001574.  
XX PR 14-JAN-2000; 2000US-00483672.

XX PA (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;  
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;  
PI Wang A, Mesgher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for diagnosing,  
PT monitoring and treating prostate cancer in a patient and for use in  
PT vaccines.

XX Claim 1; Page 493; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode  
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,  
CC and can be used in vaccine production and gene therapy. (I), (II),  
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells  
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and  
CC the antibodies are also used in the detection of cancer in a patient. The  
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)  
CC and (II) can be used in vaccines. The antibodies or (I) can be used for  
CC monitoring the progression of cancer in a patient. (I) and (II) can also  
CC be used to improve diagnostic and therapeutic methods for prostate  
CC cancer. They can indicate the level of metastasis as well as the prostate  
CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent  
CC polynucleotide and amino acid sequences used in the exemplification of

CC the present invention  
 XX  
 SQ Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;  
 Query Match 5.4%; Score 216; DB 4; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3655 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714  
 DB 7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66  
 QY 3715 ATTGACAGCGCAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCG 3774  
 DB 67 ATTGACAGCGCAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCG 126  
 QY 3775 TATGTTTTGCTGCAAAATAAGAGAGCGCTATTTTACAGATGTTGCAACACTGGGCAAG 3834  
 DB 127 TATGTTTTGCTGCAAAATAAGAGAGCGCTATTTTACAGATGTTGCAACACTGGGCAAG 186  
 QY 3835 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 3870  
 DB 187 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 222  
 RESULT 7  
 AAS64133  
 ID AAS64133 standard; cDNA; 291 BP.  
 AC AAS64133;  
 XX  
 DT 29-JAN-2002 (first entry)  
 DE Human cDNA encoding prostate protein P510S-C.  
 XX  
 KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.  
 XX  
 OS Homo sapiens.  
 OS Microbacterium; tuberculosis.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 PN WO200173032-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 27-MAR-2001; 2001WO-US009919.  
 XX  
 PR 27-MAR-2000; 2000US-00536857.  
 PR 09-MAY-2000; 2000US-00568100.  
 PR 12-MAY-2000; 2000US-00570737.  
 PR 13-JUN-2000; 2000US-00593793.  
 PR 27-JUN-2000; 2000US-00605783.  
 PR 09-AUG-2000; 2000US-00636215.  
 PR 06-SEP-2000; 2000US-00651236.  
 PR 02-OCT-2000; 2000US-00657279.  
 PR 10-OCT-2000; 2000US-00679426.  
 PR 09-NOV-2000; 2000US-00709729.  
 XX  
 (CORI-) CORIXA CORP.  
 XX  
 XU J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
 Panger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
 Li SX, Wang A, Skeiky YAW, Hepier WT, Henderson RA;  
 WPI; 2001-639232/73.  
 DR P-PSDB; AAU69900.  
 XX  
 PT New human prostate-specific polypeptides and polynucleotides useful for  
 the diagnosis and treatment of cancer, especially prostate cancer.  
 XX  
 PS Claim 1; Page 533; 579pp; English.

XX The invention relates to isolated prostate-specific polynucleotides,  
 CC polypeptides, fusion proteins of the polypeptides, antibodies raised  
 CC against the polypeptides (or antigenic epitopes derived from them) and  
 CC antigen-presenting cells expressing the polypeptides. The antibodies are  
 CC useful for detecting the presence of cancer, especially prostate cancer.  
 CC The polypeptides, polynucleotides and the antigen-presenting cells are  
 CC useful for stimulating and/or expanding T cells specific for a tumour  
 CC protein, and for inhibiting the development of cancer especially prostate  
 CC cancer. Compositions comprising the polynucleotide and/or polypeptide are  
 CC useful for stimulating an immune response, and for treating cancer. The  
 CC oligonucleotide is useful for detecting cancer. The present sequence is a  
 CC prostate specific polynucleotide of the invention  
 XX  
 SQ Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;  
 Query Match 5.4%; Score 216; DB 4; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3655 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714  
 DB 7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66  
 QY 3715 ATTGACAGCGCAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCG 3774  
 DB 67 ATTGACAGCGCAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCG 126  
 QY 3775 TATGTTTTGCTGCAAAATAAGAGAGCGCTATTTTACAGATGTTGCAACACTGGGCAAG 3834  
 DB 127 TATGTTTTGCTGCAAAATAAGAGAGCGCTATTTTACAGATGTTGCAACACTGGGCAAG 186  
 QY 3835 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 3870  
 DB 187 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 222  
 RESULT 8  
 ACA59941  
 ID ACA59941 standard; cDNA; 291 BP.  
 XX  
 AC ACA59941;  
 XX  
 DT 10-JUN-2003 (first entry)  
 DE Prostate cancer therapy associated cDNA #648.  
 XX  
 KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;  
 KW immunogen; cancer; prostate specific antigen; PSA;  
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;  
 KW PSMA; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002192763-A1.  
 XX  
 PD 19-DEC-2002.  
 XX  
 PF 29-JUN-2001; 2001US-00895793.  
 XX  
 PR 04-OCT-1999; 99US-0157455P.  
 PR 04-OCT-2000; 2000US-00679272.  
 PR 28-MAR-2001; 2001US-00822827.  
 XX  
 (XUJ)/ XU J.  
 PA (DILL)/ DILLON D C.  
 PA (MITC)/ MITCHAM J L.  
 PA (HARL)/ HARLOCKER S L.  
 PA (JIANG)/ JIANG Y.  
 PA (KALOS)/ KALOS M D.  
 PA (FANG)/ FANGER G R.  
 PA (RETT)/ RETTER M W.  
 PA (STOL)/ STOLK J A.

PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;  
PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;  
XX  
DR WPI; 2001-245062/25.  
XX  
XX Prostate specific protein and its encoding polynucleotide, useful for the  
PT treatment and diagnosis of prostate cancer.  
PT  
XX Disclosure; SEQ ID NO 823; 85pp; English.  
XX  
CC The invention describes a fusion protein comprising at least one amino  
CC acid sequence of immunogenic portions of any of the 3 sequences not  
CC defined in the specification, or sequences having at least 70 or 90 %  
CC sequence identity to any one of the 35 sequences defined in the USPTO web  
CC site, which is encoded by any of the 4 nucleotide sequences not defined  
CC in the specification. The fusion protein, composition and methods are  
CC useful for diagnosing, preventing and/or treating cancer, particularly  
CC prostate cancer. The proteins are useful as markers to indicate the  
CC presence or absence of cancer. This sequence represents a prostate cancer  
CC therapy associated cDNA. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from the US patent office at  
CC seqdata.uspto.gov/sequence.html?docID=US20020192763  
XX  
XX Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;  
SQ

Query Match 5.4%; Score 216; DB 5; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCACTGCACCGTGTCTAACCATTTGCACACAGATTGAACACCAT 3714  
Db 7 ATCCGGGAGAAATTTGCCACTGCACCGTGTCTAACCATTTGCACACAGATTGAACACCAT 66

Qy 3715 ATTGACAGCGACAAGATAATGGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCG 3774  
Db 67 ATTGACAGCGACAAGATAATGGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCG 126

Qy 3775 TATGTTTTCGCAAAATTAAGAGAGCCCTATTTTACAGATGGTGCAACACTGGGCAAG 3834  
Db 127 TATGTTTTCGCAAAATTAAGAGAGCCCTATTTTACAGATGGTGCAACACTGGGCAAG 186

Qy 3835 GCAGAGCGCGTGCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAGCGCGTGCCTCACTGAAACAGCAAAACAG 222

RESULT 9  
ID ABL95504  
XX ABL95504 standard; cDNA; 291 BP.  
AC ABL95504;  
XX  
XX 29-AUG-2003 (revised)  
DT 19-JUL-2002 (first entry)  
XX  
XX P510S-C construct cDNA sequence SEQ ID NO 823.

XX  
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;  
KW gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
OS Chimeric.  
XX  
PN US2002022248-A1.  
XX  
PD 21-FEB-2002.  
XX  
XX 12-JAN-2001; 2001US-00759143.  
XX  
PR 25-FEB-1997; 97US-00806099.  
PR 01-AUG-1997; 97US-00904804.  
PR 10-FEB-1998; 98US-00020956.  
PR 25-FEB-1998; 98US-00030607.  
PR 14-JUL-1998; 98US-00115453.  
PR 23-SEP-1998; 98US-00159812.  
PR 15-JAN-1999; 99US-00232149.  
PR 09-APR-1999; 99US-00288946.  
PR 13-JUL-1999; 99US-00352616.  
PR 12-NOV-1999; 99US-00439313.  
PR 18-NOV-1999; 99US-00443686.  
PR 14-JAN-2000; 2000US-00483672.  
PR 27-MAR-2000; 2000US-00536857.  
PR 09-MAY-2000; 2000US-00568100.  
PR 12-MAY-2000; 2000US-00570737.  
PR 13-JUN-2000; 2000US-00593793.  
PR 27-JUN-2000; 2000US-00605783.  
PR 10-AUG-2000; 2000US-00636215.  
PR 29-AUG-2000; 2000US-00651236.  
PR 08-SEP-2000; 2000US-00657279.  
PR 02-OCT-2000; 2000US-00679426.  
PR 10-OCT-2000; 2000US-00685166.  
XX  
XX (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
XX  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
XX  
XX WPI; 2002-255649/30.  
XX  
XX New prostate-specific polynucleotides for diagnosing and treating  
PT diseases, in particular prostate cancer, and as markers for the  
PT progression of cancer.  
XX  
XX Claim 1; SEQ ID NO 823; 87pp; English.  
XX  
CC The present invention provides prostate-specific coding sequences and  
CC their encoded proteins. These can be used in the diagnosis and treatment  
CC of cancers, particularly prostate cancer. The present sequence is a cDNA  
CC described in the invention. (Updated on 29-AUG-2003 to standardise OS  
CC field)  
XX  
XX Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;  
SQ

```
Query Match 5.4%; Score 216; DB 6; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.1e-96;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGACAAGATAATGTTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCG 3774
Db 67 ATTGACAGCGACAAGATAATGTTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGAGCCTATTTTACAAGATGGTGCAACTGGGCAAG 3834
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGAGCCTATTTTACAAGATGGTGCAACTGGGCAAG 186

Qy 3835 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db 187 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 222
```

```
RESULT 10
ACC95668
ID ACC95668 standard; cDNA; 291 BP.
XX
AC ACC95668;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific cDNA sequence SEQ ID 823.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillion DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Ranger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De Bassolec, Foy TW, Watanabe Y;
PI Deng T;
XX
DR WPI; 2003-167130/16.
XX
XX New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
XX Example 17; Page 602; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
XX Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;
```

```
Query Match 5.4%; Score 216; DB 8; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.1e-96;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGACAAGATAATGTTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCG 3774
Db 67 ATTGACAGCGACAAGATAATGTTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGAGCCTATTTTACAAGATGGTGCAACTGGGCAAG 3834
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGAGCCTATTTTACAAGATGGTGCAACTGGGCAAG 186

Qy 3835 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 3870
Db 187 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 222
```

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RESULT 11
ADB14273
ID ADB14273 standard; cDNA; 291 BP.
XX
AC ADB14273;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific protein P5108-construct C cDNA.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell; gene; fusion protein.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
```

XX PA (CORI-) CORIXA CORP.  
 XX PI Xu J, Stolk JA, Kalos MD;  
 XX DR WPI; 2003-756193/71.  
 XX DR P-PSDB; ADB14276.  
 XX PT New isolated polypeptide for use in a vaccine for stimulating an immune  
 PT response, or for treating or diagnosis cancer, preferably prostate  
 PT cancer.  
 XX XX  
 PS Example 17; Page; 101pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide comprising no more than  
 CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The  
 CC peptides comprise a fragment ADB13563 of that contain naturally processed  
 CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)  
 CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific  
 CC cDNA, one of 648 disclosed as new. Also included are nucleic acids  
 CC encoding the proteins and peptides, expression vectors, a host cell  
 CC transformed with the vector, an isolated antibody (or antigen binding  
 CC fragment) that specifically binds to the protein or peptide, detecting  
 CC the presence of a cancer in a patient (comprising contacting a patient  
 CC sample with a binding agent that binds to the peptides or a polypeptide  
 CC appearing as ADB1358, detecting the amount of polypeptide that binds to  
 CC the agent and comparing the amount of polypeptide to a predetermined cut-  
 CC off value to determine the presence of cancer), a fusion protein  
 CC comprising the peptides or proteins, stimulating or expanding T cells  
 CC specific for a tumour protein comprising contacting T cells with the  
 CC peptides or the isolated T cell population, treating prostate cancer in a  
 CC patient comprising administering a composition comprising the peptides,  
 CC nucleic acids, antibodies or compounds, determining the presence of a  
 CC cancer in a patient and treating prostate cancer in a patient comprising  
 CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated  
 CC from a patient with the peptides or antigen presenting cells that express  
 CC the peptides so that the T cells proliferate, and administering the  
 CC proliferated T cells to the patient. The peptides (or an oligonucleotide  
 CC that hybridises to nucleic acid encoding them), is used to detect the  
 CC presence of cancer in a patient. The peptides, nucleic acids encoding, or  
 CC antigen-presenting cells expressing the nucleic acid, are used to  
 CC stimulate or expand T cells specific for a tumour protein. The peptides,  
 CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen  
 CC presenting cells are used to stimulate an immune response or treat  
 CC prostate cancer in a patient. The present sequence is a cDNA encoding a  
 CC fusion protein comprising a prostate specific protein. Note: Except where  
 CC otherwise indicated, the sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030185830.  
 XX  
 SQ Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;  
 Query Match 5.4%; Score 216; DB 10; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3655 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACATTGCACACAGTGAACACCAT 3714  
 Db 7 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACATTGCACACAGTGAACACCAT 66  
 Qy 3715 ATTCACAGCGACAGATTAATGTTTATGATTTCAGAGACTGAAGATATGATGACCG 3774  
 Db 67 ATTCACAGCGACAGATTAATGTTTATGATTTCAGAGACTGAAGATATGATGACCG 126  
 Qy 3775 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAGATGTTGCAACAACTGGCAAG 3834  
 Db 127 TATGTTTGTCTGCAAAATAAAGAGAGCGCTATTTTACAGATGTTGCAACAACTGGCAAG 186  
 Qy 3835 GCAGAGCGCGTGCCTCAGTGAACAGCAAAACAG 3870  
 Db 187 GCAGAGCGCGTGCCTCAGTGAACAGCAAAACAG 222

RESULT 12  
 ADG26689  
 ID ADG26689 standard; cDNA; 291 BP.  
 XX  
 AC ADG26689;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Human prostate-specific cDNA #665.  
 XX  
 KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;  
 KW cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2003157089-A1.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PP 09-MAY-2002; 2002US-00144678.  
 XX  
 PR 25-FEB-1997; 97US-00806099.  
 PR 01-AUG-1997; 97US-00904804.  
 PR 09-FEB-1998; 98US-00020956.  
 PR 25-FEB-1998; 98US-00030607.  
 PR 14-JUL-1998; 98US-00115453.  
 PR 23-SEP-1998; 98US-00159812.  
 PR 15-JAN-1999; 99US-00232149.  
 PR 09-APR-1999; 99US-00288946.  
 PR 13-JUL-1999; 99US-0032616.  
 PR 12-NOV-1999; 99US-00439313.  
 PR 18-NOV-1999; 99US-00443686.  
 PR 14-JAN-2000; 2000US-00483672.  
 PR 27-MAR-2000; 2000US-00536857.  
 PR 09-MAY-2000; 2000US-00568100.  
 PR 13-JUN-2000; 2000US-00570737.  
 PR 12-JUN-2000; 2000US-00593793.  
 PR 27-JUN-2000; 2000US-00605783.  
 PR 09-AUG-2000; 2000US-00636215.  
 PR 29-AUG-2000; 2000US-00651236.  
 PR 06-SEP-2000; 2000US-00657279.  
 PR 02-OCT-2000; 2000US-00679426.  
 PR 10-OCT-2000; 2000US-00685166.  
 PR 09-NOV-2000; 2000US-00709729.  
 PR 12-JAN-2001; 2001US-00759143.  
 PR 09-FEB-2001; 2001US-00780669.  
 PR 09-MAY-2001; 2001US-00852911.  
 PR 29-JUN-2001; 2001US-00895814.  
 PR 10-DEC-2001; 2001US-00012896.  
 XX  
 (CORI-) CORIXA CORP.  
 XX  
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;  
 PI Kalos MD, Fanger CR, Retter MW, Stolk JA, Day CH, Vedwick TS;  
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;  
 PI McNeill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;  
 PI Meagher MJ, Deng T;  
 XX  
 WPI; 2003-777973/73.  
 DR P-PSDB; ADG26692.  
 XX  
 PT New polynucleotides encoding prostate specific polypeptides isolated from  
 PT a human prostate tumor cDNA library are useful to diagnose and treat  
 PT cancer particularly prostate cancer.  
 XX  
 PS Example 17; SEQ ID NO 823; 99pp; English.  
 XX  
 CC The invention relates to human prostate-specific polypeptides and the  
 CC polynucleotides encoding them. The invention also relates to an isolated  
 CC antibody or its antigen-binding fragment that specifically binds a  
 CC polypeptide of the invention, a method of detecting cancer in a patient  
 CC comprising contacting a biological sample of the patient with an agent  
 CC that binds a prostate-specific polypeptide and comparing the amount of



bound polypeptide compared to a predetermined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents cDNA encoding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

Sequence 291 BP; 92 A; 71 C; 68 G; 60 T; 0 U; 0 Other;  
Query Match 5.4%; Score 216; DB 10; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3655 ATCCGGAGAAATTTGCCACTGCACCGTGTAAACCAATTGCACAGATTCAACACCAATT 3714  
Db 7 ATCCGGAGAAATTTGCCACTGCACCGTGTAAACCAATTGCACAGATTCAACACCAANTT 66  
Qy 3715 ATTGACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCG 3774  
Db 67 ATTGACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCG 126  
Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACACTGGGCAAG 3834  
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACACTGGGCAAG 186  
Qy 3835 GCAGAAGCGCGTGCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCGCGTGCCTCACTGAAACAGCAAAACAG 222

RESULT 13  
AAX40493  
ID AAX40493 standard; cDNA; 439 BP.  
XX AAX40493;  
AC AAX40493;  
XX AAX40493;  
DT 18-JUN-1999 (first entry)  
XX Human secreted protein 5' EST SEQ ID No: 93.  
DE Human; secreted protein; EST; expressed sequence tag; diagnosis;  
KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;  
KW upstream regulatory sequence; cytokine activity; cell proliferation;  
KW differentiation; haematopoiesis regulation; tissue growth regulation;  
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;  
KW thrombolytic; anti-inflammatory; tumour inhibition; db.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO9906550-A2.  
PN WO9906550-A2.  
XX 11-FEB-1999.  
PD 31-JUL-1998; 98WO-IB001232.  
PF 01-AUG-1997; 97US-00905144.  
XX (GBST ) GENSET.  
FA Dumas Milne Edwards J, Duclert A, Lacroix B;  
XX WPI; 1999-153780/13.  
DR P-PSDB; RAY11771.  
XX New isolated prostate-derived nucleic acids - used to develop products  
PT which may have cytokine, immune regulatory, haematopoiesis regulating,  
PT anti-inflammatory or tumour inhibition activity.  
XX Claim 1; Page 214-215; 675pp; English.  
PS AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for  
XX human secreted proteins expressed in prostate, and encode the proteins

given in AAY11716 to AAY11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell

XX  
SQ Sequence 439 BP; 128 A; 89 C; 96 G; 122 T; 0 U; 4 Other;  
Query Match 5.3%; Score 211; DB 2; Length 439;  
Best Local Similarity 100.0%; Pred. No. 3.6e-94;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2040 GAATGTCCTCCAGTTACACTATCAGAGGAGAACCCCTCTGAGGAAAGTGGTTTCAGGC 2099  
Db 229 GAATGTCCTCCAGTTACACTATCAGAGGAGAACCCCTCTGAGGAAAGTGGTTTCAGGC 288  
Qy 2100 CTATAAGAATTTACTTTCAGAGCTGGTCTCACTGGATTGTCTTCATTTTCTTCTCTCT 2159  
Db 289 CTATAAGAATTTACTTTCAGAGCTGGTCTCACTGGATTGTCTTCATTTTCTTCTCTCT 348  
Qy 2160 AAACACTGCAGCTCAGGTTGCTTATGCTTCAAGATTGGTGGCTTTCATATCTGGGCAA 2219  
Db 349 AAACACTGCAGCTCAGGTTGCTTATGCTTCAAGATTGGTGGCTTTCATATCTGGGCAA 408  
Qy 2220 CAACAAGATGCTAAATGCTACTGTAAT 2250  
Db 409 CAACAAGATGCTAAATGCTACTGTAAT 439

RESULT 14  
ABV41670  
ID ABV41670 standard; cDNA; 391 BP.  
XX ABV41670;  
AC ABV41670;  
XX 16-SEP-2002 (first entry)  
DT Human prostate expression marker cDNA 41661.  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
DE Human; pharmacogenomic marker; gene; ss.  
KW Homo sapiens.  
OS Homo sapiens.  
XX WO200160860-A2.  
PN WO200160860-A2.  
XX 23-AUG-2001.  
PD 20-FEB-2001; 2001WO-US005171.  
PF 17-FEB-2000; 2000US-0183319P.  
XX 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
FA Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
DR  
XX

PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.

XX PS  
XX Claim 1; Page 8367; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 391 BP; 101 A; 88 C; 94 G; 108 T; 0 U; 0 Other;

Query Match 5.3%; Score 210; DB 5; Length 391;

Best Local Similarity 100.0%; Pred. No. 1.1e-93;

Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 532 GCATTCGTCTTACTACATGGCCATGGGGAGACCAACAGCCAGATAGTCAATCTG 591

Db 167 GCATTCGTCTTACTACATGGCCATGGGGAGACCAACAGCCAGATAGTCAATCTG 226

Qy 592 CTGTCCCAATGATGTGAACAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGGGCA 651

Db 227 CTGTCCCAATGATGTGAACAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGGGCA 286

Qy 652 GGACCACTGACGGGATCGCAGTGCCTCTACTCTGGATGGAGATAGGAATATCGTGC 711

Db 287 GGACCACTGACGGGATCGCAGTGCCTCTACTCTGGATGGAGATAGGAATATCGTGC 346

Qy 712 CTTCCTGGGATGGCAGTCTTAATCATCTC 741

Db 347 CTTCCTGGGATGGCAGTCTTAATCATCTC 376

RESULT 15

ID ABV32629 standard; cDNA; 444 BP.

XX AC ABV32629;

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 32620.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-0183319P.

XX 16-MAR-2000; 2000US-0189862P.

XX 25-MAY-2000; 2000US-0207454P.

XX 09-JUN-2000; 2000US-0211314P.

XX 18-JUL-2000; 2000US-0219007P.

XX 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 6954; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 444 BP; 110 A; 97 C; 113 G; 124 T; 0 U; 0 Other;

Query Match 5.2%; Score 208; DB 5; Length 444;

Best Local Similarity 100.0%; Pred. No. 1.1e-92;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 568 ACCACAGGCCAGATAGTCAATCTCTCTCCCAATGATGTGAACAGTTTGTATCAGGTGACA 627

Db 225 ACCACAGGCCAGATAGTCAATCTCTCTCCCAATGATGTGAACAGTTTGTATCAGGTGACA 284

Qy 628 GTGTTCTTACACTTCTCTGGCAGGACCACTCGCAGGCGATCGCAGTGCCTTACTC 687

Db 285 GTGTTCTTACACTTCTCTGGCAGGACCACTCGCAGGCGATCGCAGTGCCTTACTC 344

Qy 688 TGGATGGAGATAGGAATATCTGCTTGGGATGGCAGTTCTTAATCATCTTCTCTGCC 747

Db 345 TGGATGGAGATAGGAATATCTGCTTGGGATGGCAGTTCTTAATCATCTTCTCTGCC 404

Qy 748 TTGCAAAAGCTGTTTGGGAAAGTTGTTCT 775

Db 405 TTGCAAAAGCTGTTTGGGAAAGTTGTTCT 432

Search completed: May 19, 2005, 19:10:11

Job time : 1987 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2005, 03:57:21 ; Search time 620 Seconds  
(without alignments)  
10498.563 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcccgtgtaccagga.....ttttcgagacagcactgtga 3978

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3973.2	99.9	4231	4	US-09-647-140B-1
2	3966	99.7	6082	3	US-09-439-313-535
3	3966	99.7	6082	4	US-09-636-215-535
4	3966	99.7	6082	4	US-09-685-166A-535
5	3966	99.7	6082	4	US-09-679-426-535
6	3966	99.7	6082	4	US-09-759-143-535
7	3966	99.7	6082	4	US-09-651-236-535
8	3977.8	95.5	6140	3	US-09-439-313-536
9	3977.8	95.5	6140	4	US-09-636-215-536
10	3977.8	95.5	6140	4	US-09-685-166A-536
11	3977.8	95.5	6140	4	US-09-679-426-536
12	3977.8	95.5	6140	4	US-09-759-143-536
13	3977.8	95.5	6140	4	US-09-651-236-536
14	1047	26.3	1074	4	US-09-636-215-824
15	1047	26.3	1074	4	US-09-685-166A-824
16	1047	26.3	1074	4	US-09-679-426-824
17	1047	26.3	1074	4	US-09-759-143-824
18	1047	26.3	1074	4	US-09-651-236-824
19	517	13.0	553	4	US-09-281-646B-27
20	517	13.0	2275	4	US-09-281-646B-1
21	435.8	11.0	4781	2	US-09-001-273-1
22	435.8	11.0	4781	3	US-08-843-459A-1
23	435.8	11.0	4847	3	US-09-061-400-1
24	435.8	11.0	5838	4	US-09-647-140B-3
25	431.2	10.8	586	4	US-09-281-646B-14
26	428.6	10.8	5696	4	US-09-976-594-335
27	390.4	9.8	5011	1	US-08-141-893-1

28	390.4	9.8	5011	1	US-08-463-092B-1	Sequence 1, Appli
29	390.4	9.8	5011	2	US-08-462-109A-1	Sequence 1, Appli
30	390.4	9.8	5011	2	US-08-460-907B-1	Sequence 1, Appli
31	390.4	9.8	5011	3	US-08-463-179A-1	Sequence 1, Appli
32	390.4	9.8	5011	3	US-08-461-384B-1	Sequence 1, Appli
33	390.4	9.8	5011	3	US-08-407-207A-1	Sequence 1, Appli
34	388.8	9.8	5011	1	US-08-463-092B-3	Sequence 3, Appli
35	388.8	9.8	5011	2	US-08-462-109A-3	Sequence 3, Appli
36	388.8	9.8	5011	2	US-08-460-907B-3	Sequence 3, Appli
37	388.8	9.8	5011	3	US-08-463-179A-3	Sequence 3, Appli
38	388.8	9.8	5011	3	US-08-461-384B-3	Sequence 3, Appli
39	377	9.5	5889	1	US-08-463-092B-5	Sequence 5, Appli
40	377	9.5	5889	2	US-08-462-109A-5	Sequence 5, Appli
41	377	9.5	5889	2	US-08-460-907B-5	Sequence 5, Appli
42	377	9.5	5889	3	US-08-463-179A-5	Sequence 5, Appli
43	377	9.5	5889	3	US-08-461-384B-5	Sequence 5, Appli
44	367	9.2	5232	3	US-08-972-927-1	Sequence 1, Appli
45	356.2	9.0	5175	3	US-08-972-927-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-647-140B-1  
; Sequence 1, Application US/09647140B  
; Patent No. 6803184  
; GENERAL INFORMATION:  
; APPLICANT: Fox Chase Cancer Center  
; APPLICANT: Kruh, Gary D.  
; APPLICANT: Lee, Kun  
; APPLICANT: Belinsky, Martin G.  
; APPLICANT: Bain, Lisa J.  
; TITLE OF INVENTION: WEP-Related ABC Transporter Encoding  
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof  
; FILE REFERENCE: FCCC 98-02  
; CURRENT APPLICATION NUMBER: US/09/647,140B  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: PCT/US99/06644  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,759  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/095,153  
; PRIOR FILING DATE: 1998-08-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4231  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-647-140B-1

Query Match	99.9%	Score	3973.2	DB	4	Length	4231
Best Local Similarity	99.9%	Pred. No.	0				
Matches	3975	Conservative	0	Mismatches	3	Indels	0
Gaps	0						
Qy	1	ATGTCGCCGTGTACAGGAGGTCAAGCCCAACCGCTGCAGGACGCGAACTCTGCTCA	60				
Db	116	ATGTCGCCGTGTACAGGAGGTCAAGCCCAACCGCTGCAGGACGCGAACTCTGCTCA	175				
Qy	61	CGCGTGTCTTCTCGTGGCTCAATCCCTGTTTAAATTTGCCCATAAACGGAGATTAGAG	120				
Db	176	CGCGTGTCTTCTCGTGGCTCAATCCCTGTTTAAATTTGCCCATAAACGGAGATTAGAG	235				
Qy	121	GAAGATGATGATGATTCAGTCTGCCAGAGACCGCTCAGACGACCTTGGAGAGATTG	180				
Db	236	GAAGATGATGATGATTCAGTCTGCCAGAGACCGCTCAGACGACCTTGGAGAGATTG	295				
Qy	181	CAAGGGTTCGGGATAAGAGTTTAAAGCTCAGATGACGACAGACCTTCTTTA	240				
Db	296	CAAGGGTTCGGGATAAGAGTTTAAAGCTCAGATGACGACAGACCTTCTTTA	355				
Qy	241	ACAAGAGCAATCATAAAGTGTACTGGAAATCTTATTATTAGTTTGGGAATTTTACGTTA	300				

Db 356 ACAGAGCAATCATAAAGTGTACTGGAACTTATTTAGTTTGGGAAATTTTACGTTA 415  
Qy 301 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTTT 360  
Db 416 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTTT 475  
Qy 361 GAAATTTATGATCCCATGGATTCTGTGGCTTTGAAACACAGGTTACGGCTATGCCACGGTG 420  
Db 476 GAAATTTATGATCCCATGGATTCTGTGGCTTTGAAACACAGGTTACGGCTATGCCACGGTG 535  
Qy 421 CTGACTTTTTTGCAGCGCTCAATTTTGGCTATACTGCAATCACTATATATTTTATCAGTTTCAG 480  
Db 536 CTGACTTTTTTGCAGCGCTCAATTTTGGCTATACTGCAATCACTATATATTTTATCAGTTTCAG 595  
Qy 481 TGTGCTCGGATAGAGTTACGATAGCCATGTCATATGATTTTATCGAAAGGCACTTCGT 540  
Db 596 TGTGCTCGGATAGAGTTACGATAGCCATGTCATATGATTTTATCGAAAGGCACTTCGT 655  
Qy 541 CTTAGTAAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT 600  
Db 656 CTTAGTAAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT 715  
Qy 601 GATGTGAACAAGTTTGTATCAGTGCACAGTGTCTTACATCTCTGTCGGCAGGACCACTG 660  
Db 716 GATGTGAACAAGTTTGTATCAGTGCACAGTGTCTTACATCTCTGTCGGCAGGACCACTG 775  
Qy 661 CAGCGATCGCAGTGAATCGCCCTACTCTGGATGAGATAGAAATPATCGTGCCTTGTGGG 720  
Db 776 CAGCGATCGCAGTGAATCGCCCTACTCTGGATGAGATAGAAATPATCGTGCCTTGTGGG 835  
Qy 721 ATGGCAGTTCTAATCATCTCTGCCCTTGCAGAGCTTTTGGGAAGTTTGTCTCATCA 780  
Db 836 ATGGCAGTTCTAATCATCTCTGCCCTTGCAGAGCTTTTGGGAAGTTTGTCTCATCA 895  
Qy 781 CTGAGGAGTAAATCGCAACTTTTCACGATGCCAGGATCAGGACCATGAATGAAGTTATA 840  
Db 896 CTGAGGAGTAAATCGCAACTTTTCACGATGCCAGGATCAGGACCATGAATGAAGTTATA 955  
Qy 841 ACTGGTATAAGGATPAATAAAATGTACGCCCTGGGAAAAGTCATTTTCAAATCTTATTACC 900  
Db 956 ACTGGTATAAGGATPAATAAAATGTACGCCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015  
Qy 901 AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAAGTTCTCTGCCCTCAGGGGATGAAT 960  
Db 1016 AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAAGTTCTCTGCCCTCAGGGGATGAAT 1075  
Qy 961 TTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTGTGTGACCTTCACCACCTACGTG 1020  
Db 1076 TTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTGTGTGACCTTCACCACCTACGTG 1135  
Qy 1021 CTCCTCGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080  
Db 1136 CTCCTCGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195  
Qy 1081 GTGGGGCTGACGGTTACCTCTTCTCCCTCAGCCATTTGAGAGGGTGTGAGAGGCAATC 1140  
Db 1196 GTGGGGCTGACGGTTACCTCTTCTCCCTCAGCCATTTGAGAGGGTGTGAGAGGCAATC 1255  
Qy 1141 GTCAGCATCCGAGAAATCCAGACCTTTTGTCTACTGATGAGATATCACAGCGCAACCGT 1200  
Db 1256 GTCAGCATCCGAGAAATCCAGACCTTTTGTCTACTTGTGATGAGATATCACAGCGCAACCGT 1315  
Qy 1201 CAGCTGCCGTGAGATGGTAAAGATGGTGCATGTGACAGGATTTTACTGCTTTTTGGGAT 1260  
Db 1316 CAGCTGCCGTGAGATGGTAAAGATGGTGCATGTGACAGGATTTTACTGCTTTTTGGGAT 1375  
Qy 1261 AAGCATCAGAGACCCCACTCTACAGGCCCTTTCTTTACTGTACAGACCTGGCGAATTG 1320  
Db 1376 AAGCATCAGAGACCCCACTCTACAGGCCCTTTCTTTACTGTACAGACCTGGCGAATTG 1435  
Qy 1321 TTAGCTGTGGTCCGCCCGTGGGAGCAGGGAAGTCATCAGTGTAAAGTGGCGGTCTCGGG 1380

Db 1436 TTAGCTGTGGTCCGCCCGTGGGAGCAGGGAAGTCATCACTGTAAAGTCGCTGCTCGG 1495  
Qy 1381 GAATTTGGCCCCCAAGTCACGGGCTGGTCAGCGTCGATGGGAAGATTTGCTATGTGCTCAG 1440  
Db 1496 GAATTTGGCCCCCAAGTCACGGGCTGGTCAGCGTCGATGGGAAGATTTGCTATGTGCTCAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
Db 1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615  
Qy 1501 AAGGAAACGATATGAAAAAGTCATAAAGGCTTGTCTCTGAAAAAGGATTTACAGCTGTG 1560  
Db 1616 AAGGAAACGATATGAAAAAGTCATAAAGGCTTGTCTCTGAAAAAGGATTTACAGCTGTG 1675  
Qy 1561 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAA 1620  
Db 1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAA 1735  
Qy 1621 GCACGGGTAAACCTTGCACAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGAAGAT 1680  
Db 1736 GCACGGGTAAACCTTGCACAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGAAGAT 1795  
Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
Db 1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855  
Qy 1741 ATTTTGCATCAGAAAGATCACAATTTTGTAGTCACTCATCAGTTGCAATGCTCAAGCTGCA 1800  
Db 1856 ATTTTGCATCAGAAAGATCACAATTTTGTAGTCACTCATCAGTTGCAATGCTCAAGCTGCA 1915  
Qy 1801 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGGTGCAGAAAGGGACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGGTGCAGAAAGGGACTTACACTGAGTTC 1975  
Qy 1861 CTAAATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAAATAGGAAAGTGAAACAA 1920  
Db 1976 CTAAATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAAATAGGAAAGTGAAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980  
Db 2036 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095  
Qy 1981 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2040  
Db 2096 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2155  
Qy 2041 AATGTCCAGTTCACACTATCAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCC 2100  
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Db 2216 TATAAGAAATTTACTTTCAGAGCTGGTGTCTACTGGATTTGTCTTTCATTTTCTTCTCCTTA 2275  
Qy 2161 AACACTCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTCATATCTGGGCAAAAC 2220  
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Qy 2221 AAAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAAGCTAGAT 2280  
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Qy 2281 CTTAACTGGTACTTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGGCATA 2340  
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Qy 2341 GCAAGATCTCTATTTGGTATTTCTAGTCTCTTGTAACTCTTCACAAAACCTTTCACAAAACAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTTCTAGTCTCTTGTAACTCTTCACAAAACCTTTCACAAAACAA 2515  
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Qy 121 GAAGATGATATGTAATTCAGTGCTGCCAGAGACCGCTCAGAGCACCTTGGAGGAGTTG 180  
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Db 366 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTCAGAGATCAGCAGACAGAGCCCTTCCTTA 425  
Qy 241 ACAAGAGCAATCATPAAGTGTACTGGAAATCTTAATTTAGTTTGGGAAATTTTACGTTA 300  
Db 426 ACAAGAGCAATCATPAAGTGTACTGGAAATCTTAATTTAGTTTGGGAAATTTTACGTTA 485  
Qy 301 ATTGAGGAAAGTGCACAAAGTAATCCAGCCCAATTTTTGGGAAAATTAATTAATTTT 360  
Db 486 ATTGAGGAAAGTGCACAAAGTAATCCAGCCCAATTTTTGGGAAAATTAATTAATTTT 545  
Qy 361 GAAATTTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 420  
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Qy 421 CTGACTTTTTGCACGCTCATTTTGGCTATATCTGCATCACTTATATTTTATFCAGTTTCAG 480  
Db 606 CTGACTTTTTGCACGCTCATTTTGGCTATATCTGCATCACTTATATTTTATFCAGTTTCAG 665  
Qy 481 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACCTTCGT 540  
Db 666 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACCTTCGT 725  
Qy 541 CTTAGTAACATGGCCATGGGGAGACAAACACAGCCAGATAGTCAATCTGCTGTCCAAT 600  
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Db 846 CAGCGATCGCAGTAGCCTACTCTGATGAGATAGGAATATCGTGGCTTGTCTGGG 905  
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Db 906 ATGCGAGTTCTAAATCATTTCTCCCTTGCACAAAGCTTTTGGGAAAGTTGTTCTCATCA 965  
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Db 966 CTGAGGAGTAAACTGCAACTTTTCAAGATGCCAGATCAGGACCATGAATGAAGTTTATA 1025  
Qy 841 ACTGGTATAGGATAATAAATAATGATAGCCTGGGAAAAGTCAATTTCAAATCTTATTACC 900  
Db 1026 ACTGGTATAGGATAATAAATAATGATAGCCTGGGAAAAGTCAATTTCAAATCTTATTACC 1085  
Qy 901 AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAAGTTCTCCCTCAGGGGATGAAT 960  
Db 1086 AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAAGTTCTCCCTCAGGGGATGAAT 1145  
Qy 961 TTGGCTTTCTGTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCAACCACCTACGTG 1020  
Db 1146 TTGGCTTTCTGTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCAACCACCTACGTG 1205  
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Db 1326 GTCAGCATCCGAGAAATCCAGACTTTTGTGCTATTGATGAGATATCACAGCGCAACCGT 1385

Qy 1201 CAGCTGCCGTGATGCTAAAGATGCTGCATGTCAGGATTTTACTGCTTTTGGAT 1260  
Db 1386 CAGCTGCCGTGATGCTAAAGATGCTGCATGTCAGGATTTTACTGCTTTTGGAT 1445  
Qy 1261 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTTACTGTACAGCTTGGCGAATTG 1320  
Db 1446 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTTACTGTACAGCTTGGCGAATTG 1505  
Qy 1321 TTAGCTGTGTGCGGCCCGTGGGAGCAGGGAAGTCACTACCTGTAAAGTGGCTCGG 1380  
Db 1506 TTAGCTGTGTGCGGCCCGTGGGAGCAGGGAAGTCACTACCTGTAAAGTGGCTCGG 1565  
Qy 1381 GAATTGSCCCCAAGTCAAGGCTGTGTCAGCTGATGGAAGAAATGCTTACTCTCAG 1440  
Db 1566 GAATTGSCCCCAAGTCAAGGCTGTGTCAGCTGATGGAAGAAATGCTTACTCTCAG 1625  
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Qy 1501 AAGGAACGATATGAAGAAAGTCAAGGCTTGTCTCTGAAAAGGATTTACAGCTGTTG 1560  
Db 1686 AAGGAACGATATGAAGAAAGTCAAGGCTTGTCTCTGAAAAGGATTTACAGCTGTTG 1745  
Qy 1561 GAGGATGCTGATCTGACTGTGATAGGAGATCGGGGAACACGCTGAGTGGAGGCGAGAA 1620  
Db 1746 GAGGATGCTGATCTGACTGTGATAGGAGATCGGGGAACACGCTGAGTGGAGGCGAGAA 1805  
Qy 1621 GCACGGGTAAACCTTGCACAGCAGCTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1680  
Db 1806 GCACGGGTAAACCTTGCACAGCAGCTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1865  
Qy 1681 CCTCTCAGTCCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
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Db 1986 AGTCAGATTTCTGATTAATTAAGATGTTAAATGTTGTCAGAGGAGGACTTACACTGAGTTC 2045  
Qy 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGATTAATGAGAAAGTGAACAA 1920  
Db 2046 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGTAAATGAGAAAGTGAACAA 2105  
Qy 1921 CCTCCAGTCCAGGAACTCCACACTAAGAACTCGTACCTTCTCAGAGTCTTCGGTTTGG 1980  
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Qy 1981 TCTCAACAATCTTCTAGACCTCTCTGAAAAGATGGTCTCTGGAGAGCCCAAGATACAGAG 2040  
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Qy 2101 TATAAGAAATTAATTTACAGAGTGGTCTCACTGGATTGTCTTCAATTTCTTATTTCTCTTA 2160  
Db 2286 TATAAGAAATTAATTTACAGAGTGGTCTCACTGGATTGTCTTCAATTTCTTATTTCTCTTA 2345  
Qy 2161 AACACTGCAGTCAAGTTGCTTATGCTTTCAAGATTTGGTGGCTTTTATCTGGGCAAC 2220  
Db 2346 AACACTGCAGTCAAGTTGCTTATGCTTTCAAGATTTGGTGGCTTTTATCTGGGCAAC 2405  
Qy 2221 AAACAAAGTATGCTAAATGCTCACTGTAATTCGAGGAGGAATGTAAACGAGAACTAGAT 2280  
Db 2406 AAACAAAGTATGCTAAATGCTCACTGTAATTCGAGGAGGAATGTAAACGAGAACTAGAT 2465  
Qy 2281 CTTAACTGGTACTTAGGAAATTTTATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCAT 2340

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Db      |||||CTTAACTGGTACTTAGGAATTTATCTAGGTTTAACTGTAGTACCGTTCTTTTGGCATA 2525
Qy      |||||GCAAGATCTCTATTGGTATTCTAGTCTCTGTTAACTCTTACAAACTTTTGCACAACAA 2400
Db      |||||GCAAGATCTCTATTGGTATTCTAGTCTCTGTTAACTCTTACAAACTTTTGCACAACAA 2585
Qy      |||||ATGTTTCAGTCAATTTCTGAAAGCTCCGGTATTATTCTTTGATGAAATCCAAATAGGAAGA 2460
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Qy      |||||TTTTTCCACATTTGTCATCTCTCTCCAGGGCTCTGGACCATCCGGGCATCAAAAGCAGAA 2760
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Qy      |||||GAGAGGTGTGAGGAACGTTTGTGATGACACACAGGATTTACATTCAGAGGCTTGTCTCTTG 2820
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Db      |||||AAAGAGCACCTTGGGAATATCAGAACGCCACCCAGCCTGGCCCATGAGGAGTG 3305
Qy      |||||ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGTGACTGAAGCAT 3180
Db      |||||ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGTGACTGAAGCAT 3365
Qy      |||||CTGACAGCATCTAATTAATCACAAGAAAGTTGGCAATTTGGGAAGAACCCGAGCTGGA 3240
Db      |||||CTGACAGCATCTAATTAATCACAAGAAAGTTGGCAATTTGGGAAGAACCCGAGCTGGA 3425
Qy      |||||AAAAGTTCCTCATCTCAGCCCTTTTAGATTGTCAGAACCCGAGTAAATTTGGATT 3300
Db      |||||AAAAGTTCCTCATCTCAGCCCTTTTAGATTGTCAGAACCCGAGTAAATTTGGATT 3485
Qy      |||||GATAAGATCTTGACAACTGAAATTTGACTTCAAGATTTAAGGAAGAAATGTCAATCATA 3360
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Qy      |||||CCTCAGGAACCTGTTTGTTCCTGGAAACATGAGGAAACCTGGATCCCTTTAATGAG 3420
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Db      |||||CCTCAGGAACCTGTTTGTTCCTCAGGAACATGAGGAAAACTGGATCCCTTTAATGAG 3605
Qy      |||||CACACGATGAGGAACCTGTTGAAATGCTTACAAAGGTTACAACTTAAAGAAACCATTTGAA 3480
Db      |||||CACACGATGAGGAACCTGTTGAAATGCTTACAAAGGTTACAACTTAAAGAAACCATTTGAA 3665
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Db      |||||GATCTTCTCGTAAAAATGGATACCTGAATTTAGCAGAAATCAGATCCAAATTTTAGTGTGGA 3725
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Db      |||||CAAAAGAACCTGTTGCTGCTTGCAGGGCAATTTCTCAGGAAAAATCAGATTTGATTTATT 3785
Qy      |||||GATGAACGCGACGGCAAAATGTTGATCCAAAGAACTGATGATTTAATAC-AAAAAATCCGG 3660
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Qy      |||||GAGAAATTTGCCCACTGACCGTCTAACCAATTTGCACACAGATTTGAACACCATTTATTGAC 3720
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## RESULT 3

US-09-636-215-535

; Sequence 535, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

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; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 535



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:   LENGTH: 6082
:   TYPE: DNA
:   ORGANISM: Homo sapiens
US-09-636-215-535

Query Match      99.7%;   Score 3966;   DB 4;   Length 6082;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 3977;   Conservative 0;   Mismatches 0;   Indels 1;   Gaps 1;

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Qy   61   CGCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAATTTGGCCATAACCGAGATTAGAG   120
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Qy   121   GAAGATGATATGTAATTCAGTGTCTCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG   180
Db   306   GAAGATGATATGTAATTCAGTGTCTCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG   365

Qy   181   CAAGGGTTCGGGATAAAGAGTTTAAAGAGCTGAGAAATGACGACAGAAAGCCCTTTCTTTA   240
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Db   426   ACAAGACCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA   485

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Qy   361   GAAATATTATGATCCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCTATGCCACGGTG   420
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Db   846   CAGCGGATCGCAGTGACTGCCCTTACTCTGGATGGAGATAGGAATATCGTGCCTTGTCTGGG   905

Qy   721   ATGGAGTCTTAATCAATCTCTGCGCCCTTGCAGAGCTGTTTTGGGAAGTTGTTCTCATCA   780
Db   906   ATGGAGTCTTAATCAATCTCTGCGCCCTTGCAGAGCTGTTTTGGGAAGTTGTTCTCATCA   965

Qy   781   CTGAGGAGTAAACGTGCACTTTTCCGGATGCCAGGATCAGGACCAATGAATGAAGTTATA   840
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Qy   841   ACTGGTATAAGGATAAATAAATGTACGCCCTGGGAAAGTCAATTTCAAATCTTATTACC   900
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Qy   901   AATTGTGAGAAAGAGGAGATTTCCAAGATTTCTGAGAGTTCTCTGCTCAGGGGAGATGAAT   960
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Qy   961   TTGGCTTCGTTTTTTTCAGTGCAGCAAAATCATCTGTGTTTGTGACCTTCCACCACCTACGTG   1020
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Qy   1021   CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATATGGGGCT   1080
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Qy   1081   GTGGCGGTGACGGTTACCTTCTTCCCTCAGCCATTCAGAGGGGTGTGAGAGGCAATC   1140
Db   1266   GTGGCGGTGACGGTTACCTTCTTCCCTCAGCCATTCAGAGGGGTGTGAGAGGCAATC   1325

Qy   1141   GTCAGCATCCGAAGAATCCAGAGCCCTTTTCTACTTCATGATGAGATATCACAGCGCAACCGT   1200
Db   1326   GTCAGCATCCGAAGAATCCAGAGCCCTTTTCTACTTCATGATGAGATATCACAGCGCAACCGT   1385

Qy   1201   CAGCTGCGGTGATGATGTTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT   1260
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Qy   1261   AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTACTGTACAGACCTGGGCAATTG   1320
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Qy   1321   TTAGCTGTGTGTCGCGCCCGCTGGGAGCAGGGAAGTCACTACCTGTTAAGTGCCTGCTCGGG   1380
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Qy   1381   GAATTGCGCCCAAGTCACTGCGGCTGGTGCAGCGTGCATGGAAGAAATTCAGCTGTCTCAG   1440
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Qy   1441   CAGCCCTGGGTGTCTCGGNACTCTGAGGAGTAATATTTTATTTGGGAGAAATACAGAA   1500
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Db   1746   GAGGATGGTGTGATCTGACTGTGATAGGAGATCGGGGAACCCAGCTGAGTGGAGGCGAGAA   1805

Qy   1621   GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT   1680
Db   1806   GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT   1865

Qy   1681   CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA   1740
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Db   1926   ATTTTGCATGAGAAAGATCAAAATTTTAGTGACTCATCAGTTTGCAGTACCTCAAAAGCTGCA   1985

Qy   1801   AGTCAGATTCTGATATTTGAAAGATGTTAAATGTCGAGAGGGGACTTACACTGAGTTC   1860
Db   1986   AGTCAGATTCTGATATTTGAAAGATGTTAAATGTCGAGAGGGGACTTACACTGAGTTC   2045

Qy   1861   CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGGAAAGTCAACAA   1920
Db   2046   CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGGAAAGTCAACAA   2105

Qy   1921   CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG   1980
Db   2106   CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG   2165

Qy   1981   TCTCAAACAATCTTCTAGACCTCTCTGAAAGATGTCCTCTGGAGAGCACAAGATACAGAG   2040
Db   2166   TCTCAAACAATCTTCTAGACCTCTCTGAAAGATGTCCTCTGGAGAGCACAAGATACAGAG   2225

Qy   2041   AATGTCCAGTTTACACTATCAGAGGAGAACCGTTTCTGAAGGAAAAAGTTGGTTTTCAGGCC   2100

```



[illegible]

Db	3306	ATAATCTTTGACAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGTGTACTGAAGCAT	3366
Qy	3181	CTGACAGCACTCATTAATAATCAACAAGAAAGGTTGGCAATGTGGGAAGAACCGAGAGCTGGA	3240
Db	3366	CTGACAGCACTCATTAATAATCAACAAGAAAGGTTGGCAATGTGGGAAGAACCGAGAGCTGGA	3425
Qy	3241	AAAAGTTCCTCATCTCAGCCCTTTTGTAGATCTCAGAACCCGAAGGTAAATTTTGGATT	3300
Db	3426	AAAAGTTCCTCATCTCAGCCCTTTTGTAGATCTCAGAACCCGAAGGTAAATTTTGGATT	3485
Qy	3301	GATAAGATCTTGACAACTGAAATTTGGACTTTCACGATTTAAGGAAGAAAAATGTCAATCATATA	3360
Db	3486	GATAAGATCTTGACAACTGAAATTTGGACTTTCACGATTTAAGGAAGAAAAATGTCAATCATATA	3545
Qy	3361	CCTCAGGAACCTGTTTGTTCACCTGGAACAATGAGGAAACCACTGGATCCCTTTAATGAG	3420
Db	3546	CCTCAGGAACCTGTTTGTTCACCTGGAACAATGAGGAAACCACTGGATCCCTTTAATGAG	3605
Qy	3421	CACACGGATGAGGAACGTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA	3480
Db	3606	CACACGGATGAGGAACGTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA	3665
Qy	3481	GATCTTCTCGTAAAAATGGATACTGTAATTAGCAGAACTCAGGATCCAATTTTAGTGTGGA	3540
Db	3666	GATCTTCTCGTAAAAATGGATACTGTAATTAGCAGAACTCAGGATCCAATTTTAGTGTGGA	3725
Qy	3541	CAAAAGCAACTGGTGTGCTTGGCCAGCGGCAATCTCAGGAAAAATCAGATATTGATTAATT	3600
Db	3726	CAAAAGCAACTGGTGTGCTTGGCCAGCGGCAATCTCAGGAAAAATCAGATATTGATTAATT	3785
Qy	3601	GATGAACGACGGCAAAATGTGGAATCCAAGAACTGATGAGTTAATACAAAAAAAATCCCG	3660
Db	3786	GATGAACGACGGCAAAATGTGGAATCCAAGAACTGATGAGTTAATACAAAAAAAATCCCG	3844
Qy	3661	GAGAAATTTGCCCACTGCACCGTGCTAAACATTTGCAACAGATTTGAACCACTATTATGAC	3720
Db	3845	GAGAAATTTGCCCACTGCACCGTGCTAAACATTTGCAACAGATTTGAACCACTATTATGAC	3904
Qy	3721	AGCGCAAGATATAGTTTTTGTAGATTCAGGAAGACTCGAAAGMATATCATGAGCCGATGTT	3780
Db	3905	AGCGCAAGATATAGTTTTTGTAGATTCAGGAAGACTCGAAAGMATATCATGAGCCGATGTT	3964
Qy	3781	TTGCTGCAAAATAAAGAGAGCCCTATTTTTACAAGATGGTGCACAACTGGCGAAGGACAGAA	3840
Db	3965	TTGCTGCAAAATAAAGAGAGCCCTATTTTTACAAGATGGTGCACAACTGGCGAAGGACAGAA	4024
Qy	3841	GCGCTGCCCTCACTGAAACAGCAAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT	3900
Db	4025	GCGCTGCCCTCACTGAAACAGCAAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT	4084
Qy	3901	GGTCACACTGACCACATGGTTTACAAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT	3960
Db	4085	GGTCACACTGACCACATGGTTTACAAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT	4144
Qy	3961	TTGAGACAGCACTGTGA	3978
Db	4145	TTGAGACAGCACTGTGA	4162

RESULT 4  
US-09-685-166A-535  
; Sequence 535, Application US/09685166A  
; Patent No. 6630305  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedrick, Thomas S.  
; APPLICANT: Carter, Barrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER  
; CURRENT APPLICATION NUMBER: US/09/685,166A  
; CURRENT FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 898  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 535  
; LENGTH: 6082  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-685-166A-535

Query Match 99.7%; Score 3966; DB 4; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	1	ATGCTGCCCGTGTACCAAGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA	60
Db	186	ATGCTGCCCGTGTACCAAGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA	245
Qy	61	CGCGTGTCTTCTCGTGGCTCAATCCCTTGTAAAAATTTGGCCATAAACGGAGATTAGAG	120
Db	246	CGCGTGTCTTCTCGTGGCTCAATCCCTTGTAAAAATTTGGCCATAAACGGAGATTAGAG	305
Qy	121	GAAGATGATATGTAATCAGTGTGCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG	180
Db	306	GAAGATGATATGTAATCAGTGTGCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG	365
Qy	181	CAAGGTTCTGGGATAAGAGTTTAAAGCTGAGATGAGATGACGACAGAGCCCTCTTTTA	240
Db	366	CAAGGTTCTGGGATAAGAGTTTAAAGCTGAGATGAGATGACGACAGAGCCCTCTTTTA	425
Qy	241	ACAAGAGCAATCATAAAGTGTACTGGAAATCTTAATTTAGTTTGGAAATTTTACGTTA	300
Db	426	ACAAGAGCAATCATAAAGTGTACTGGAAATCTTAATTTAGTTTGGAAATTTTACGTTA	485
Qy	301	ATTGAGGAAAGTGCCAAAGTAATCCAGCCCAATTTTGGGAAAAATTAATAATATTTT	360
Db	486	ATTGAGGAAAGTGCCAAAGTAATCCAGCCCAATTTTGGGAAAAATTAATAATATTTT	545
Qy	361	GAAATATATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG	420
Db	546	GAAATATATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG	605
Qy	421	CTGACTTTTTCACGCTCAATTTGGCTATCTGCATCACTATATATTTTATACGTTTACG	480
Db	606	CTGACTTTTTCACGCTCAATTTGGCTATCTGCATCACTATATATTTTATACGTTTACG	665
Qy	481	TGTCCTGGGATGAGGTTACGATAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT	540
Db	666	TGTCCTGGGATGAGGTTACGATAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT	725
Qy	541	CTTAGTAACATGGCCATGGGGAAGACCAACACAGCCAGATAGTCAATCTGCTGCCAAT	600
Db	726	CTTAGTAACATGGCCATGGGGAAGACCAACACAGCCAGATAGTCAATCTGCTGCCAAT	785
Qy	601	GATGTGAACAAGTTTGTATCAGGTACAGTGTCTTACACTTCTCTGTGGGAGGACCACTG	660
Db	786	GATGTGAACAAGTTTGTATCAGGTACAGTGTCTTACACTTCTCTGTGGGAGGACCACTG	845
Qy	661	CAGCGATCGCAGTACGTCCTACTCTGGATGGAGATAGGAATPATCGTGCCTTGTGGG	720
Db	846	CAGCGATCGCAGTACGTCCTACTCTGGATGGAGATAGGAATPATCGTGCCTTGTGGG	905

Qy	721	ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAAGAGCTGTTTTGGAAAGTTGTTCTCATCA	780
Db	906	ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAAGAGCTGTTTTGGAAAGTTGTTCTCATCA	965
Qy	781	CTGAGGAGTAAAACTGCAACTTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA	840
Db	966	CTGAGGAGTAAAACTGCAACTTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA	1025
Qy	841	ACTGGTATAAGGATATAAAAAATGACGCTGGGAAAAAGTCATTTTCAAACTCTATTACC	900
Db	1026	ACTGGTATAAGGATATAAAAAATGACGCTGGGAAAAAGTCATTTTCAAACTCTATTACC	1085
Qy	901	AATTTGAGAAAGAGGAGATTTCGAAGTTCTGAGAAAGTTTCCTGCCCTCAGGGGATGAAT	960
Db	1086	AATTTGAGAAAGAGGAGATTTCGAAGTTCTGAGAAAGTTTCCTGCCCTCAGGGGATGAAT	1145
Qy	961	TTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTGTTTGACCTTTCACCACTACGTG	1020
Db	1146	TTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTGTTTGACCTTTCACCACTACGTG	1205
Qy	1021	CTCCTCGGAGTGTGATCACAGCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGCT	1080
Db	1206	CTCCTCGGAGTGTGATCACAGCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGCT	1265
Qy	1081	GTGCGGCTGACGGTTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC	1140
Db	1266	GTGCGGCTGACGGTTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC	1325
Qy	1141	GTCAAGCATCCGAAGAAATCCAGACCTTTTCTACTTCTGATGAGATATCACAGCGCAACCGT	1200
Db	1326	GTCAAGCATCCGAAGAAATCCAGACCTTTTCTACTTCTGATGAGATATCACAGCGCAACCGT	1385
Qy	1201	CAGTCGCCGTGAGATGCTGTAAGAGATGCTGATGTCAGGATTTTACTGCTTTTGGAT	1260
Db	1386	CAGTCGCCGTGAGATGCTGTAAGAGATGCTGATGTCAGGATTTTACTGCTTTTGGAT	1445
Qy	1261	AAGCATCAGAGACCCCAACTCTACAGGCGCTTCTTCTTACTGTACAGACTGGCGAATTG	1320
Db	1446	AAGCATCAGAGACCCCAACTCTACAGGCGCTTCTTCTTACTGTACAGACTGGCGAATTG	1505
Qy	1321	TTAGCTGTGTGTCGGCCCCGTGGGAGCAGGAAAGTCATCACTGTGTTAAGTCGCTCGGG	1380
Db	1506	TTAGCTGTGTGTCGGCCCCGTGGGAGCAGGAAAGTCATCACTGTGTTAAGTCGCTCGGG	1565
Qy	1381	GAATTTGCCCCCAAGTCACGGCTGCTGATGTCAGGAGATTTGCTATGCTCTCAG	1440
Db	1566	GAATTTGCCCCCAAGTCACGGCTGCTGATGTCAGGAGATTTGCTATGCTCTCAG	1625
Qy	1441	CAGCCCTGGGTGTTCTCGGAACTCTGAGGAGTAATAATTTTATTTGGAAAGAAATACGAA	1500
Db	1626	CAGCCCTGGGTGTTCTCGGAACTCTGAGGAGTAATAATTTTATTTGGAAAGAAATACGAA	1685
Qy	1501	AAGGAAACGATATGAAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTG	1560
Db	1686	AAGGAAACGATATGAAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTG	1745
Qy	1561	GAGGATGCTGATCTGATGATAGGAGATCGGGAAACCAAGCTGAGTGAGGGCAGAAA	1620
Db	1746	GAGGATGCTGATCTGATGATAGGAGATCGGGAAACCAAGCTGAGTGAGGGCAGAAA	1805
Qy	1621	GCACGGTAAACCTTTCAGAGCAGCTGATCAAGATCTGACATCTATCTCTCGACGAT	1680
Db	1806	GCACGGTAAACCTTTCAGAGCAGCTGATCAAGATCTGACATCTATCTCTCGACGAT	1865
Qy	1681	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA	1740
Db	1866	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA	1925
Qy	1741	ATTTTGATGAGAGATCACAATTTTAGTGAATCATCAGTGTGACGTACCTCAAGCTGCA	1800
Db	1926	ATTTTGATGAGAGATCACAATTTTAGTGAATCATCAGTGTGACGTACCTCAAGCTGCA	1985
Qy	1801	AGTCAGATTTCTGATATTTGAAAGATGGTAAAAATGGTGCAAGGGGACTTTACACTGAGTTC	1860

[illegible]

Db	3066	ATCATCGTGTGCCCTTTGGGTCCCTGATTTCTGGCAAAAACCTCTGGATCGCCGGCAGGTTGGT	3120
Qy	2941	TTGGCACTGCTCATATGCCCTCAGCGCTCATGGGATGTTTCAGTGGTGTTGTTCAGCAAAAGT	3000
Db	3126	TTGGCACTGCTCATATGCCCTCAGCGCTCATGGGATGTTTCAGTGGTGTTGTTCAGCAAAAGT	3185
Qy	3001	GCTGAAGTTGAGAATATGATGATCTCAGTAGAAGGGTCANTGAATACACAGACCTTGAA	3060
Db	3186	GCTGAAGTTGAGAATATGATGATCTCAGTAGAAGGGTCANTGAATACACAGACCTTGAA	3245
Qy	3061	AAAGAACGACTTTGGGNAATACAGAAACGCCACCCAGCCCTGGCCCATGAAGAGATG	3120
Db	3246	AAAGAACGACTTTGGGNAATACAGAAACGCCACCCAGCCCTGGCCCATGAAGAGATG	3305
Qy	3121	ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT	3180
Db	3306	ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT	3365
Qy	3181	CTGACAGCACTCAATTAATCAAGAAGAGTTGGCAATTTGTGGGAAGAACCCGAGCTGGA	3240
Db	3366	CTGACAGCACTCAATTAATCAAGAAGAGTTGGCAATTTGTGGGAAGAACCCGAGCTGGA	3425
Qy	3241	AAAAGTCCCTCATCTCAGGCCCTTTTGTAGATTTGTTCAGAACCCGAGGTAATAATTTGGATT	3300
Db	3426	AAAAGTCCCTCATCTCAGGCCCTTTTGTAGATTTGTTCAGAACCCGAGGTAATAATTTGGATT	3485
Qy	3301	GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCATTA	3360
Db	3486	GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCATTA	3545
Qy	3361	CCTCAGGAACCTGTTTGTCTACTGGAAACAAAGAGAAACCTCGATCCCTTTAATGAG	3420
Db	3546	CCTCAGGAACCTGTTTGTCTACTGGAAACAAAGAGAAACCTCGATCCCTTTAATGAG	3605
Qy	3421	CACACGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTAAGAAACCATTGAA	3480
Db	3606	CACACGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTAAGAAACCATTGAA	3665
Qy	3481	GATCTTCTCGTAAATTTGGAATCTGAAATAGCAGAAATCAGGATCCAAATTTTACTGTTGGA	3540
Db	3666	GATCTTCTCGTAAATTTGGAATCTGAAATAGCAGAAATCAGGATCCAAATTTTACTGTTGGA	3725
Qy	3541	CAAGAACAACCTGGTGTGCTTGCAGGGCAATTTCTCAGGAATAATCAGATATTGATTATT	3600
Db	3726	CAAGAACAACCTGGTGTGCTTGCAGGGCAATTTCTCAGGAATAATCAGATATTGATTATT	3785
Qy	3601	GATGAAGCAGCGCAAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAATCCCG	3660
Db	3786	GATGAAGCAGCGCAAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAATCCCG	3844
Qy	3661	GAGAAATTTGCCCACTGCACCGTGCTAACCTATGGCACACAGATTGGAACCACTATTATGAC	3720
Db	3845	GAGAAATTTGCCCACTGCACCGTGCTAACCTATGGCACACAGATTGGAACCACTATTATGAC	3904
Qy	3721	AGCGACAAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTAATTT	3780
Db	3905	AGCGACAAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTAATTT	3964
Qy	3781	TTGCTGCAAAATAAAGAGAGCCCTATTTTTACAAGATGGTGCAACAACCTGGGCAAGCAGAA	3840
Db	3965	TTGCTGCAAAATAAAGAGAGCCCTATTTTTACAAGATGGTGCAACAACCTGGGCAAGCAGAA	4024
Qy	3841	GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAGAAATTTATCCACATATT	3900
Db	4025	GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAGAAATTTATCCACATATT	4084
Qy	3901	GGTCACACTGACCACATGGTTTACAAACCTTCCAATGGACAGCCCTCGACCTTTAACTATT	3960
Db	4085	GGTCACACTGACCACATGGTTTACAAACCTTCCAATGGACAGCCCTCGACCTTTAACTATT	4144
Qy	3961	TTGAGACAGCACTGTGA	3978
Db	4145	TTGAGACAGCACTGTGA	4162

## RESULT 5

US-09-679-426-535

; Sequence 535, Application US/09679426

; Patent No. 6759515

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqui

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Barrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C20

; CURRENT APPLICATION NUMBER: US/09/679,426

; CURRENT FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 895

; SOFTWARE: Fast-Seq for Windows Version 3.0

; SEQ ID NO 535

; LENGTH: 6082

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-679-426-535

Query Match 99.7%; Score 3966; DB 4; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	481	TGTGCTGGGATGAGTTTACGAGTAGCATCTGTCATATGATTTATCGAAAGGCACCTTCGT	540
Db	666	TGTGCTGGGATGAGTTTACGAGTAGCATCTGTCATATGATTTATCGAAAGGCACCTTCGT	725
Qy	541	CTTAGTAACATGCCCATGGGAAAGACAAACACAGGCCAGATAGTCAATCTGCTGTCCAAT	600
Db	726	CTTAGTAACATGCCCATGGGAAAGACAAACACAGGCCAGATAGTCAATCTGCTGTCCAAT	785
Qy	601	GATGTGAAACAAGTTTGATCAGGTGACAGTGTCTTACACTCTCTGTCGGCAGGACCACTG	660
Db	786	GATGTGAAACAAGTTTGATCAGGTGACAGTGTCTTACACTCTCTGTCGGCAGGACCACTG	845
Qy	661	CAGCCGATCGCAGTACTGCTTACTCTGATGGAGATAGAAATATCTGTCCTTCTGCTGGG	720
Db	846	CAGCCGATCGCAGTACTGCTTACTCTGATGGAGATAGAAATATCTGTCCTTCTGCTGGG	905
Qy	721	ATGGCAGTTCTTAATCAATTCCTGCCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTA	780
Db	906	ATGGCAGTTCTTAATCAATTCCTGCCCTTGCCTTGCCTTGCCTTGCCTTGCCTA	965
Qy	781	CTGAGGATGTAACCTGCACTTTTCAAGGATGCCAGATCAGGATCAGGACCAATGAATGAT	840
Db	966	CTGAGGATGTAACCTGCACTTTTCAAGGATGCCAGATCAGGATCAGGACCAATGAATGAT	1025
Qy	841	ACTGGTATAAGGATATAAAATGTACGCTCGGAAAGTCAATTTTCAAAATCTTATTTACC	900
Db	1026	ACTGGTATAAGGATATAAAATGTACGCTCGGAAAGTCAATTTTCAAAATCTTATTTACC	1085
Qy	901	AATTTGAGAAAGAGGAGATTTTCAAGATTTCTGAGAAAGTTTCTGCTTCAAGGAGATGA	960
Db	1086	AATTTGAGAAAGAGGAGATTTTCAAGATTTCTGAGAAAGTTTCTGCTTCAAGGAGATGA	1145
Qy	961	TTGGCTTCGTTTTCAGTGCAAGCAAAATCATCTGTTGTTGAGCTTTTCAACCACTAGTG	1020
Db	1146	TTGGCTTCGTTTTCAGTGCAAGCAAAATCATCTGTTGTTGAGCTTTTCAACCACTAGTG	1205
Qy	1021	CTCTCGGCAGTGTGATCAGCCAGCCGCTGTTCTGTCAGTGCAGCTGTATGCGGCT	1080
Db	1206	CTCTCGGCAGTGTGATCAGCCAGCCGCTGTTCTGTCAGTGCAGCTGTATGCGGCT	1265
Qy	1081	GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC	1140
Db	1266	GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC	1325
Qy	1141	GTGAGCATCCGAGAAATCCAGACCTTTTCTGCTACTGATGAGATATCACAGCGCAACGT	1200
Db	1326	GTGAGCATCCGAGAAATCCAGACCTTTTCTGCTACTGATGAGATATCACAGCGCAACGT	1385
Qy	1201	CAGCTGCCGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG	1260
Db	1386	CAGCTGCCGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG	1445
Qy	1261	AAGGCATCAGAGACCCCAACTCTACAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1320
Db	1446	AAGGCATCAGAGACCCCAACTCTACAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1505
Qy	1321	TTAGCTGTGTCGGCCCCCGTGGGAGCAGGAAAGTCACTGTTAACTGCGCTCGCTCGG	1380
Db	1506	TTAGCTGTGTCGGCCCCCGTGGGAGCAGGAAAGTCACTGTTAACTGCGCTCGCTCGG	1565
Qy	1381	GAATTGGCCCAAGTCACTGCGGCTGTTGATGTTGATGTTGATGTTGATGTTGATGTTG	1440
Db	1566	GAATTGGCCCAAGTCACTGCGGCTGTTGATGTTGATGTTGATGTTGATGTTGATGTTG	1625
Qy	1441	CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAATATTTTATTTTGGGAGAAATAGCA	1500
Db	1626	CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAATATTTTATTTTGGGAGAAATAGCA	1685
Qy	1501	AAGGAACGATATGAAAGTCAATAAGCTTGTCTCTGAAAGAGGATTTTACAGCTGTG	1560
Db	1686	AAGGAACGATATGAAAGTCAATAAGCTTGTCTCTGAAAGAGGATTTTACAGCTGTG	1745
Qy	1561	GAGGATGGTGTCTGACTGTAGGAGATCGGGGAAACCACTGCTGAGTGGAGGGCAGAAA	1620

Db 1746 GAGGATGGTGTATCTGACTGTGATAGGAGATCGGGGACCAACGCTGAGTGGAGGGCAGAAA 1805  
Qy 1621 GCACGGGTAAACCTTGGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGAGACGAT 1680  
Db 1806 GCACGGGTAAACCTTGGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGAGACGAT 1865  
Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTTGTTGCAACTGTGTATTTGTCAA 1740  
Db 1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTTGTTGCAACTGTGTATTTGTCAA 1925  
Qy 1741 ATTTTGCATGAGAGATCACAATTTTAGTGACTCATCAGTTGCGAGTACTCCTCAAGCTGCA 1800  
Db 1926 ATTTTGCATGAGAGATCACAATTTTAGTGACTCATCAGTTGCGAGTACTCCTCAAGCTGCA 1985  
Qy 1801 AGTCAGATTCTGATATTCGAAGATGGTAAATGGTGCAAGAGGGGACTTTACACTGAGTTC 1860  
Db 1986 AGTCAGATTCTGATATTCGAAGATGGTAAATGGTGCAAGAGGGGACTTTACACTGAGTTC 2045  
Qy 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAAGTGAA 1920  
Db 2046 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAAGTGAA 2105  
Qy 1921 CCTCAGTTCAGGAACCTCCACACTAAGGAATCGTACTCTCTCAGAGTCTTCGGTTTGG 1980  
Db 2106 CCTCAGTTCAGGAACCTCCACACTAAGGAATCGTACTCTCTCAGAGTCTTCGGTTTGG 2165  
Qy 1981 TCTCAACAATCTCTAGACCTCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2040  
Db 2166 TCTCAACAATCTCTAGACCTCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2225  
Qy 2041 AATGTCCCAGTTACACTATCAGAGGAGAACCGTCTCTGAAGAAAGTTGGTTTTTCAGGCC 2100  
Db 2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTCTCTGAAGAAAGTTGGTTTTTCAGGCC 2285  
Qy 2101 TATAAGAAATTAATTCAGAGCTGGTGCTCATCTGGATGTCTTCATTTCTCTTATTCCTCTA 2160  
Db 2286 TATAAGAAATTAATTCAGAGCTGGTGCTCATCTGGATGTCTTCATTTCTCTTATTCCTCTA 2345  
Qy 2161 AACACTGCAGCTCAGGTTCCTATGTGCTTCAAGATTTGGTGGCTTTCATCTGCGGCAAC 2220  
Db 2346 AACACTGCAGCTCAGGTTCCTATGTGCTTCAAGATTTGGTGGCTTTCATCTGCGGCAAC 2405  
Qy 2221 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAAACCGAGAAGCTAGAT 2280  
Db 2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAAACCGAGAAGCTAGAT 2465  
Qy 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA 2340  
Db 2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA 2525  
Qy 2341 GCAAGATCTCTATTGGTATTCTAGTCTCTGTTAACTCTTACAACTTTTGCACAA 2400  
Db 2526 GCAAGATCTCTATTGGTATTCTAGTCTCTGTTAACTCTTACAACTTTTGCACAA 2585  
Qy 2401 ATGTTTGAAGTCAATCTGAAAGCTCCGCTATTTCTTTTGTATAGAAATCCAAATAGGAAGA 2460  
Db 2586 ATGTTTGAAGTCAATCTGAAAGCTCCGCTATTTCTTTGTATAGAAATCCAAATAGGAAGA 2645  
Qy 2461 ATTTTAAATCGTTTCTCAAGAGACTTGGACACTTTGGATGATTTGCTGCGCTGACGTTT 2520  
Db 2646 ATTTTAAATCGTTTCTCAAGAGACTTGGACACTTTGGATGATTTGCTGCGCTGACGTTT 2705  
Qy 2521 TTAGATTTCAACAGACATTCGTAAGTGGTGGTGGTGGTCTCTGCGCTGCGCGTG 2580  
Db 2706 TTAGATTTCAACAGACATTCGTAAGTGGTGGTGGTGGTCTCTGCGCTGCGCGTG 2765  
Qy 2581 ATTCCTTGGATCGCAATACCTTGGTCCCTTGGAACTCATTTTCAATTTTCTTGGCGA 2640  
Db 2766 ATTCCTTGGATCGCAATACCTTGGTCCCTTGGAACTCATTTTCAATTTTCTTGGCGA 2825  
Qy 2641 TATTTTTTGGAAACGCTCAAGAGATGTGAAGCGCTCGGAATCTACAACCTCGGAGTCCAGTG 2700

Db 2826 TATTTTTTGGAAACGCTCAAGAGATGTGAAGCGCTCGGAATCTTACAACCTCGGAGTCCAGTG 2885  
Qy 2701 TTTTCCCACTTGTCTCATCTTCTCTCAGGGGCTCTGGACCATCTGGGCATACAAAGCAGAA 2760  
Db 2886 TTTTCCCACTTGTCTCATCTTCTCTCAGGGGCTCTGGACCATCTGGGCATACAAAGCAGAA 2945  
Qy 2761 GAGAGGTGTCAAGAACTGTGTTGATGTCACACAGGATTTACATTCAGAGGCTTGGTTC 2820  
Db 2946 GAGAGGTGTCAAGAACTGTGTTGATGTCACACAGGATTTACATTCAGAGGCTTGGTTC 3005  
Qy 2821 TTTTGTGACAAACGCTCCCGTGGTTCGCGTCTGATGTCGATGTCATCTGTGCTGCTTGTTC 2880  
Db 3006 TTTTGTGACAAACGCTCCCGTGGTTCGCGTCTGATGTCGATGTCATCTGTGCTGCTTGTTC 3065  
Qy 2881 ATCATCGTTGGCTTTTGGTCCCTCATCTTGTGCAAAACCTCTGGATGTCGCGGCGAGTTCGT 2940  
Db 3066 ATCATCGTTGGCTTTTGGTCCCTCATCTTGTGCAAAACCTCTGGATGTCGCGGCGAGTTCGT 3125  
Qy 2941 TTGGCACTGTCTTATGCGCTCACGCTCATGCGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3000  
Db 3126 TTGGCACTGTCTTATGCGCTCACGCTCATGCGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3185  
Qy 3001 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGTCATTTGAATACACAGACCTTGAA 3060  
Db 3186 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGTCATTTGAATACACAGACCTTGAA 3245  
Qy 3061 AAAGAAGCACCCTCGGAATATCAGAAACGCCACACAGGCTGSCCCCATGAAGAGTG 3120  
Db 3246 AAAGAAGCACCCTCGGAATATCAGAAACGCCACACAGGCTGSCCCCATGAAGAGTG 3305  
Qy 3121 ATAACTTTTGA CAATGTGAACTTTCATGTACAGTCCAGGTGGGCTCTCTGGTACTGAAGCAT 3180  
Db 3306 ATAACTTTTGA CAATGTGAACTTTCATGTACAGTCCAGGTGGGCTCTCTGGTACTGAAGCAT 3365  
Qy 3181 CTGACAGACTCATTAATACAAAGAAAGGTTGSCATTTGGGAGAAACCGGAGCTGGA 3240  
Db 3366 CTGACAGACTCATTAATACAAAGAAAGGTTGSCATTTGGGAGAAACCGGAGCTGGA 3425  
Qy 3241 AAAAGTTCCTCTCATCTCAGCCCTTTTGTAGATTTGTGAGAACCGGAGGTAATAATTTGGATT 3300  
Db 3426 AAAAGTTCCTCTCATCTCAGCCCTTTTGTAGATTTGTGAGAACCGGAGGTAATAATTTGGATT 3485  
Qy 3301 GATAAGATCTTGACAACTGAAATTTGACTTCCAGATTTAAGGAAGAAATGTCAATCAT 3360  
Db 3486 GATAAGATCTTGACAACTGAAATTTGACTTCCAGATTTAAGGAAGAAATGTCAATCAT 3545  
Qy 3361 CCTCAGGAACCTGTTTGTTCACATGAGAAACCAATGAGGAAACCTGGATCCCTTTAATGAG 3420  
Db 3546 CCTCAGGAACCTGTTTGTTCACATGAGAAACCAATGAGGAAACCTGGATCCCTTTAATGAG 3605  
Qy 3421 CACACGATGAGGAACCTGGAATGCGCTTACAAGAGGTACAACTTTAAAGAAACCAATTCGA 3480  
Db 3606 CACACGATGAGGAACCTGGAATGCGCTTACAAGAGGTACAACTTTAAAGAAACCAATTCGA 3665  
Qy 3481 GATCTTCTCTGTAATAATGGATACCTGAAATTCAGAAATCAGGATCCAATTTTAGTGTGGA 3540  
Db 3666 GATCTTCTCTGTAATAATGGATACCTGAAATTCAGAAATCAGGATCCAATTTTAGTGTGGA 3725  
Qy 3541 CAAAGACAACTGGTGTGCTTTCAGGGCAATTCAGGAAATAATCAGATATGATTTAT 3600  
Db 3726 CAAAGACAACTGGTGTGCTTTCAGGGCAATTCAGGAAATAATCAGATATGATTTAT 3785  
Qy 3601 GATCAAGCGGCAATAATGTCAGTCCAGGACTGATGATTTAATACAAATAATTCGG 3660  
Db 3786 GATCAAGCGGCAATAATGTCAGTCCAGGACTGATGATTTAATAC - AAAAATAATTCGG 3844  
Qy 3661 GAGAAATTTTGGCCACTGTCACCGTGTCTAACCTTGCACACAGATTTGAAACCACTATTATGAC 3720  
Db 3845 GAGAAATTTTGGCCACTGTCACCGTGTCTAACCTTGCACACAGATTTGAAACCACTATTATGAC 3904  
Qy 3721 AGCGAAGATAATGGTGTGTTTGTAGATTCAGGAAAGACTGAAAGAAATATGATGACCGGTATGTT 3780  
Db 3905 AGCGAAGATAATGGTGTGTTTGTAGATTCAGGAAAGACTGAAAGAAATATGATGACCGGTATGTT 3964





Db	1506	TTAGCTGTGGTCGCGCCCGTGGGACAGGGAAGTCATCACTGTTAAGTGGCGTCTCGGG	1565
Qy	1381	GAATTGGCCCCAAGTCAAGGCTGGTCAAGCTGCATGGAGAAATGGCTATGTGCTCAG	1440
Db	1566	GAATTGGCCCCAAGTCAAGGCTGGTCAAGCTGCATGGAGAAATGGCTATGTGCTCAG	1625
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGAA	1500
Db	1626	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGAA	1685
Qy	1501	AAGGAACGATATGAAAGATCAAAAGCTTGCTCTCTGAAAAGGATTTACAGCTGTTG	1560
Db	1686	AAGGAACGATATGAAAGATCAAAAGCTTGCTCTCTGAAAAGGATTTACAGCTGTTG	1745
Qy	1561	GAGGATGGTGTGATCTGATCTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA	1620
Db	1746	GAGGATGGTGTGATCTGATCTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA	1805
Qy	1621	GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT	1680
Db	1806	GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT	1865
Qy	1681	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1740
Db	1866	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1925
Qy	1741	ATTTTGATGAGAAGATCACAAATTTTGTAGTCACTCATCAGTTGTCAGTACCTCAAGAGTCGA	1800
Db	1926	ATTTTGATGAGAAGATCACAAATTTTGTAGTCACTCATCAGTTGTCAGTACCTCAAGAGTCGA	1985
Qy	1801	AGTCAGATTTCTGATPATTTGAAAGATGTTAAATAGTGTGCAAGGGGACTTACACTGAGTTC	1860
Db	1986	AGTCAGATTTCTGATPATTTGAAAGATGTTAAATAGTGTGCAAGGGGACTTACACTGAGTTC	2045
Qy	1861	CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATGAGGAAAGTGAAACAA	1920
Db	2046	CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATGAGGAAAGTGAAACAA	2105
Qy	1921	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGGTTGG	1980
Db	2106	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGGTTGG	2165
Qy	1981	TCTCAACAATCTTCTAGACCCCTCTTGAAGATGGTGTCTCTGAGAGCCCAAGATACAGAG	2040
Db	2166	TCTCAACAATCTTCTAGACCCCTCTTGAAGATGGTGTCTCTGAGAGCCCAAGATACAGAG	2225
Qy	2041	AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAGGAAAGTTGGTTTTCAGGCC	2100
Db	2226	AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAGGAAAGTTGGTTTTCAGGCC	2285
Qy	2101	TATAAGAAATTTACTTTCAGAGTGGTGTCTCAGTGGATCTCTTCAATTTTCTTATCTCCTA	2160
Db	2286	TATAAGAAATTTACTTTCAGAGTGGTGTCTCAGTGGATCTCTTCAATTTTCTTATCTCCTA	2345
Qy	2161	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTTCATACTGGGCAAC	2220
Db	2346	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTTCATACTGGGCAAC	2405
Qy	2221	AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGAAATGTAACCGAAGAGCTAGAT	2280
Db	2406	AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGAAATGTAACCGAAGAGCTAGAT	2465
Qy	2281	CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTCTCTTTTGGCATA	2340
Db	2466	CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTCTCTTTTGGCATA	2525
Qy	2341	GCAAGATCTCTATTTGGTATTTACGTCTTGTAACTCTTCAAAAATTTTGCACAAACAA	2400
Db	2526	GCAAGATCTCTATTTGGTATTTACGTCTTGTAACTCTTCAAAAATTTTGCACAAACAA	2585
Qy	2401	ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTTATTTTGTATGAAATCCAATAGGAAGA	2460

Db	2586	ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTTATTTTGTATGAAATCCAATAGGAAGA	2645
Qy	2461	ATTTTAAATCGTTTCTCAAAAGACATTTGGACACTTTGGATGATTTTGTCTGCCCTCAGCGTTT	2520
Db	2646	ATTTTAAATCGTTTCTCAAAAGACATTTGGACACTTTGGATGATTTTGTCTGCCCTCAGCGTTT	2705
Qy	2521	TTAGATTTTCATCCAGACATTTGCTCAAGTGGTTGGTGTGFTCTCTGTGGCTGTGGCCGTG	2580
Db	2706	TTAGATTTTCATCCAGACATTTGCTCAAGTGGTTGGTGTGFTCTCTGTGGCTGTGGCCGTG	2765
Qy	2581	ATTCCTTTGGATCGCAATACCTCTTGGTTCCCTCTGGAAATCAATTTTCAATTTTCTTCGGGA	2640
Db	2766	ATTCCTTTGGATCGCAATACCTCTTGGTTCCCTCTGGAAATCAATTTTCAATTTTCTTCGGGA	2825
Qy	2641	TATTTTGTGAAACGCTCAAGAGATGTGAAGCGCTCGGAATCTCAAACTCTCGAGTCCAGTG	2700
Db	2826	TATTTTGTGAAACGCTCAAGAGATGTGAAGCGCTCGGAATCTCAAACTCTCGAGTCCAGTG	2885
Qy	2701	TTTTTCCCATTTGTCACTTCTCTCAGGGGCTCTGACCAATCCCGGGCANATAAAGCAGAA	2760
Db	2886	TTTTTCCCATTTGTCACTTCTCTCAGGGGCTCTGACCAATCCCGGGCANATAAAGCAGAA	2945
Qy	2761	GAGAGGTTCAGGAACGTTTGTGATGACACACAGGATTTTACATTCAGAGGCTTGGTCTTGG	2820
Db	2946	GAGAGGTTCAGGAACGTTTGTGATGACACACAGGATTTTACATTCAGAGGCTTGGTCTTGG	3005
Qy	2821	TTTTTGAACAACGTCGCGCTGTTCCGCGTCTGATGCGCATCTGTGCCATGTGTTGTC	2880
Db	3006	TTTTTGAACAACGTCGCGCTGTTCCGCGTCTGATGCGCATCTGTGCCATGTGTTGTC	3065
Qy	2881	ATCATCGTTCCTTTGGGTCCTGATTTCTGGCAAAAACTCTGGATCCGGCAGGTTGGT	2940
Db	3066	ATCATCGTTCCTTTGGGTCCTGATTTCTGGCAAAAACTCTGGATCCGGCAGGTTGGT	3125
Qy	2941	TTGGCACTGCTTATGSCCTCAGCTCATCGGGATGTTTTCAGTGGTGTTCGCAAAAGT	3000
Db	3126	TTGGCACTGCTTATGSCCTCAGCTCATCGGGATGTTTTCAGTGGTGTTCGCAAAAGT	3185
Qy	3001	GCTGAACTTCAGGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA	3060
Db	3186	GCTGAACTTCAGGAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA	3245
Qy	3061	AAAGAAACACTTTGGGAATATCAGAAACGCCACCCAGCTGGCCCCCATGAAGAGTG	3120
Db	3246	AAAGAAACACTTTGGGAATATCAGAAACGCCACCCAGCTGGCCCCCATGAAGAGTG	3305
Qy	3121	ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGCAAGCAT	3180
Db	3306	ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGCAAGCAT	3365
Qy	3181	CTGACAGCACTCAATTAATCACAAGAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA	3240
Db	3366	CTGACAGCACTCAATTAATCACAAGAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA	3425
Qy	3241	AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTTCAGAACCCGAAGGTAATAATTTGGATT	3300
Db	3426	AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTTCAGAACCCGAAGGTAATAATTTGGATT	3485
Qy	3301	GATAAGATCTTGACAACTGAAATTTGAACTTCACGATTTTAAAGGAAGAAATGTCAATCATA	3360
Db	3486	GATAAGATCTTGACAACTGAAATTTGAACTTCACGATTTTAAAGGAAGAAATGTCAATCATA	3545
Qy	3361	CCTCAGGAACCTGTTTGTTCCTGGAACAACTGGAAGAAACCTGGATCCCTTTAATGAG	3420
Db	3546	CCTCAGGAACCTGTTTGTTCCTGGAACAACTGGAAGAAACCTGGATCCCTTTAATGAG	3605
Qy	3421	CACACGGATGAGGAACCTGTGGAAATGCTTACAAAGAGGTACAACTTAAAGAAACCATTTGAA	3480
Db	3606	CACACGGATGAGGAACCTGTGGAAATGCTTACAAAGAGGTACAACTTAAAGAAACCATTTGAA	3665
Qy	3481	GATCTTCTCGGTAAAAATGGGATCTGAAATTAGCAGAAATCAGGATCCAAATTTTAGTGTGGA	3540
Db	3666	GATCTTCTCGGTAAAAATGGGATCTGAAATTAGCAGAAATCAGGATCCAAATTTTAGTGTGGA	3725

QY 3541 CAAGACAACTGGTGTGCTTCCAGGCGCAATTCCTCAGGAAATCAGATATTGATTT 3600  
 Db 3726 CAAAGACAACTGGTGTGCTTCCAGGCGCAATTCCTCAGGAAATCAGATATTGATTT 3785  
 QY 3601 GATGAAGCGACGGCAATGTGGATCCAGAACTGATGAGTTAAATACAAAATAATCCGG 3660  
 Db 3786 GATGAAGCGACGGCAATGTGGATCCAGAACTGATGAGTTAAATAC-AAAAAATCCGG 3844  
 QY 3661 GAGAAATTTGCCACTGCACTGCGTCTAACCAATGCAACAGATTTGAACCAATTTGAC 3720  
 Db 3845 GAGAAATTTGCCACTGCACTGCGTCTAACCAATGCAACAGATTTGAACCAATTTGAC 3904  
 QY 3721 AGGACAGATTAATGTTTTAGATTCAGGAGACTGAAAGATATGATGAGCGGTATGTT 3780  
 Db 3905 AGGACAGATTAATGTTTTAGATTCAGGAGACTGAAAGATATGATGAGCGGTATGTT 3964  
 QY 3781 TTGCTGCAAAATAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3840  
 Db 3965 TTGCTGCAAAATAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024  
 QY 3841 GCGCTGCCCTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTCCACATATT 3900  
 Db 4025 GCGCTGCCCTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTCCACATATT 4084  
 QY 3901 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGAGAGCGCTTCACTTAACTATT 3960  
 Db 4085 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGAGAGCGCTTCACTTAACTATT 4144  
 QY 3961 TTCGAGACAGCACTGTGA 3978  
 Db 4145 TTCGAGACAGCACTGTGA 4162

RESULT 7

US-09-651-236-535  
 ; Sequence 535 Application US/09651236  
 ; Patent No. 6818751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.42718C18  
 ; CURRENT APPLICATION NUMBER: US/09/651.236  
 ; CURRENT FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 865  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 535  
 ; LENGTH: 6082  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-651-236-535

Query Match 99.7%; Score 3966; DB 4; Length 6082;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGCTGCCGTGTACACGAGGTTGAAGCCCAACCCGCTGCAGGACGCGAACTCTGCTCA 60  
 Db 186 ATGCTGCCGTGTACACGAGGTTGAAGCCCAACCCGCTGCAGGACGCGAACTCTGCTCA 245  
 QY 61 CGGCTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAG 120  
 Db 246 CGGCTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAG 305  
 QY 121 GAAGATGATATGATTTCAGTGTCTGCCAGAGACGGCTCAGACACCTTGGAGAGAGTTG 180  
 Db 306 GAAGATGATATGATTTCAGTGTCTGCCAGAGACGGCTCAGACACCTTGGAGAGAGTTG 365  
 QY 181 CAAGGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATCAGCACAGAGACCTTCTTTA 240  
 Db 366 CAAGGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATCAGCACAGAGACCTTCTTTA 425  
 QY 241 ACAAGAGCAATATAAGTGTCTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
 Db 426 ACAAGAGCAATATAAGTGTCTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 485  
 QY 301 ATTGAGAAAGTGCCTGAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT 360  
 Db 486 ATTGAGAAAGTGCCTGAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT 545  
 QY 361 GAAATTTATGATCCCATGGAATCTGTGGCTTTGAAACACAGCTACGCTATGCCACGGTG 420  
 Db 546 GAAATTTATGATCCCATGGAATCTGTGGCTTTGAAACACAGCTACGCTATGCCACGGTG 605  
 QY 421 CTGACTTTTTGACGCTCATTTTTGGCTTATCTGCATCACTTATATTTTATCAGTTTCA 480  
 Db 606 CTGACTTTTTGACGCTCATTTTTGGCTTATCTGCATCACTTATATTTTATCAGTTTCA 665  
 QY 481 TGTCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 540  
 Db 666 TGTCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725  
 QY 541 CTTAGTAAACATGCGCATGGGGAAGACAAACACAGGCGCAGATAGTCAATCTGCTGCCAAT 600  
 Db 726 CTTAGTAAACATGCGCATGGGGAAGACAAACACAGGCGCAGATAGTCAATCTGCTGCCAAT 785  
 QY 601 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGGGGAGGACCACTG 660  
 Db 786 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGGGGAGGACCACTG 845  
 QY 661 CAGCGATCCAGTACTGCCCTACTCTGATGGAGATAGAAATATCGTGGCTTGGTGGG 720  
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 QY 721 ATGGCAGTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAAGTTGTTCTCATCA 780  
 Db 906 ATGGCAGTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTGGGAAAGTTGTTCTCATCA 965  
 QY 781 CTGAGGATTAATACTGCAACTTTTACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840  
 Db 966 CTGAGGATTAATACTGCAACTTTTACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025  
 QY 841 ACTGGTATAGGATATAATAATGTACGCTCGGAAAGTCATTTTCAAATCTTATTAACC 900  
 Db 1026 ACTGGTATAGGATATAATAATGTACGCTCGGAAAGTCATTTTCAAATCTTATTAACC 1085  
 QY 901 AATTTGAGAAAGAGAGATTTTCAAGATTTCTGAGAAAGTTTCTGCCCTCAGGGGATGAAT 960  
 Db 1086 AATTTGAGAAAGAGAGATTTTCAAGATTTCTGAGAAAGTTTCTGCCCTCAGGGGATGAAT 1145  
 QY 961 TTGGCTTCGTTTTTTCAGTGAAGCAAAATCATCGTGTGTTGAGACCTTCAACCATCAGTG 1020  
 Db 1146 TTGGCTTCGTTTTTTCAGTGAAGCAAAATCATCGTGTGTTGAGACCTTCAACCATCAGTG 1205  
 QY 1021 CTCTCGGAGTGTGATCAGGACGCGCGTGTTCGTGGCAGTACGCTGTATGGGGCT 1080  
 Db 1206 CTCTCGGAGTGTGATCAGGACGCGCGTGTTCGTGGCAGTACGCTGTATGGGGCT 1265  
 QY 1081 GTGGGCTGACGGTTACCTCTTCTCCCTCAGCCATTGAGAGGGGTGTGAGAGGCAATC 1140



Db	1266	GTGGGCTGACGGT TACCCTCTCTCTCCCTCAGCCATTGAGAGGGTGTCAAGAGCAATC	1325
Qy	1141	GTCAGCATCCGAAGATCCAGACCTTTTGTCTACTTGTGATGAGATATCAACGGCAACCGT	1200
Db	1326	GTCAGCATCCGAAGATCCAGACCTTTTGTCTACTTGTGATGAGATATCAACGGCAACCGT	1385
Qy	1201	CAGCTGGCGTCAGATGGTAAAGATGGTGCATGTGCAGGAAATTTACTGTCTTTTGGGAT	1260
Db	1386	CAGCTGGCGTCAGATGGTAAAGATGGTGCATGTGCAGGAAATTTACTGTCTTTTGGGAT	1445
Qy	1261	AAGGCATCAGAGACCCCACTCTACAGGCCCTTTCTTTACTGTCTCAGACCTGGGCAATTG	1320
Db	1446	AAGGCATCAGAGACCCCACTCTACAGGCCCTTTCTTTACTGTCTCAGACCTGGGCAATTG	1505
Qy	1321	TTAGCTGTGGTGGCGCCGTCGGAGCAGGGAAGTCACTACCTGTTAAGTGGCGTCTCGGG	1380
Db	1506	TTAGCTGTGGTGGCGCCGTCGGAGCAGGGAAGTCACTACCTGTTAAGTGGCGTCTCGGG	1565
Qy	1381	GAATTGGCCCCCAAGTCAAGGCTGGTCAGCGTGCATGGAAGAAATGGCTATGTCTCTCAG	1440
Db	1566	GAATTGGCCCCCAAGTCAAGGCTGGTCAGCGTGCATGGAAGAAATGGCTATGTCTCTCAG	1625
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGA	1500
Db	1626	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGA	1685
Qy	1501	AAGGAACGATAGAAAAGTCATAAAGCTTGTCTCTGAAAAGGATTTACAGCTCTTG	1560
Db	1686	AAGGAACGATAGAAAAGTCATAAAGCTTGTCTCTGAAAAGGATTTACAGCTCTTG	1745
Qy	1561	GAGGATGGTGAATCTGACTGTGATAGGAGATCGGGGAACCAAGCTCAGTGGAGGCGAGAAA	1620
Db	1746	GAGGATGGTGAATCTGACTGTGATAGGAGATCGGGGAACCAAGCTCAGTGGAGGCGAGAAA	1805
Qy	1621	GCAGGGTAAACCTTGAAGAGAGTGTATCAAGATGCTGACATCTATCTCTCGGAGAT	1680
Db	1806	GCAGGGTAAACCTTGAAGAGAGTGTATCAAGATGCTGACATCTATCTCTCGGAGAT	1865
Qy	1681	CCTCTCAGTGCAGTAGATGGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1740
Db	1866	CCTCTCAGTGCAGTAGATGGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1925
Qy	1741	ATTTTGATGAGAGATACAAATTTTATGACTCATCAGTTGCTGAGTACCTCAAAAGCTGCA	1800
Db	1926	ATTTTGATGAGAGATACAAATTTTATGACTCATCAGTTGCTGAGTACCTCAAAAGCTGCA	1985
Qy	1801	AGTCAGATCTGATATTGAAAGATGGTAAATGTGTGAGAGGGGACTTACACTGAGTTC	1860
Db	1986	AGTCAGATCTGATATTGAAAGATGGTAAATGTGTGAGAGGGGACTTACACTGAGTTC	2045
Qy	1861	CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA	1920
Db	2046	CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA	2105
Qy	1921	CCTCCAGTTCAGGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG	1980
Db	2106	CCTCCAGTTCAGGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG	2165
Qy	1981	TCTCAACAAATCTTCTAGACCTCTTGAAGATGGTGTCTGGAGAGCCCAAGATACAGAG	2040
Db	2166	TCTCAACAAATCTTCTAGACCTCTTGAAGATGGTGTCTGGAGAGCCCAAGATACAGAG	2225
Qy	2041	AATGTCCAGTTACACTATCAGAGAGAACCGTTCTGAGGAAAGTGGTTTTCAGGCC	2100
Db	2226	AATGTCCAGTTACACTATCAGAGAGAACCGTTCTGAGGAAAGTGGTTTTCAGGCC	2285
Qy	2101	TATAAGAAATTTACTTTCAGAGCTGGTGTCTCAGTGAATGTCTTCAATTTTCTTCTCTTA	2160
Db	2286	TATAAGAAATTTACTTTCAGAGCTGGTGTCTCAGTGAATGTCTTCAATTTTCTTCTCTTA	2345
Qy	2161	AACAATGACGCTCAGGTTGGCTATGTGCTTCAAGATGGTGGCTTTCATATCTGGGCAAC	2220
Db		AACAATGACGCTCAGGTTGGCTATGTGCTTCAAGATGGTGGCTTTCATATCTGGGCAAC	
Db	2346	AACAATGACGCTCAGGTTGGCTATGTGCTTCAAGATGGTGGCTTTCATATCTGGGCAAC	2405
Qy	2221	AAACAAAGTATGCTTAAATGTCACTGTAAATCGAGGAGGAAATGTAAACCGAGAGCTAGAT	2280
Db	2406	AAACAAAGTATGCTTAAATGTCACTGTAAATCGAGGAGGAAATGTAAACCGAGAGCTAGAT	2465
Qy	2281	CTTAACTGGTATCTTGAAGAAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340
Db	2466	CTTAACTGGTATCTTGAAGAAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2525
Qy	2341	GCAAGATCTCTATTGGTATTCTACGTCCTGTGTTAACTCTTACAAACTTTTGCACAACTTTG	2400
Db	2526	GCAAGATCTCTATTGGTATTCTACGTCCTGTGTTAACTCTTACAAACTTTTGCACAACTTTG	2585
Qy	2401	ATGTTTCAGTCAATCTCTGAAAGCTCCCGTATATTTCTTTGATAGAAATCAATAGGAAGA	2460
Db	2586	ATGTTTCAGTCAATCTCTGAAAGCTCCCGTATATTTCTTTGATAGAAATCAATAGGAAGA	2645
Qy	2461	ATTTTAAATCGTTTCTCCAAAGACATTTGGACATCTTGGATGATTTTGTGCGCTGACGTTT	2520
Db	2646	ATTTTAAATCGTTTCTCCAAAGACATTTGGACATCTTGGATGATTTTGTGCGCTGACGTTT	2705
Qy	2521	TTAGATTTTCATCCAGACATTTGCTACAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	2580
Db	2706	TTAGATTTTCATCCAGACATTTGCTACAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	2765
Qy	2581	ATTCCTTTGGATCGCAATACCTTGGTTCCTTCCCTTGGAAATCATTTTCAATTTTCTTGGCGA	2640
Db	2766	ATTCCTTTGGATCGCAATACCTTGGTTCCTTCCCTTGGAAATCATTTTCAATTTTCTTGGCGA	2825
Qy	2641	TATTTTGGAAACGTCAGAGATGTGAAGCGCTTGGAAATCTCAACACTCGGAGTCCAGTG	2700
Db	2826	TATTTTGGAAACGTCAGAGATGTGAAGCGCTTGGAAATCTCAACACTCGGAGTCCAGTG	2885
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Qy 3901 GGTCACTGACCACTGGTTTACAAAACATTTCCAAATGGACAGCCCTCGACCTTAACTATT 3960
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RESULT 8
US-09-439-313-536
; Sequence 536, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439.313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (4535)
; OTHER INFORMATION: n=A,T,C or G
; US-09-439-313-536

Query Match      95.5%; Score 3797.8; DB 3; Length 6140;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9

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US-09-636-215-536
; Sequence 536, Application US/09636215
; Patent No. 8620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

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; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-636-215-536

Query Match          95.5%; Score 3797,8; DB 4; Length 6140;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 74 GGTGGCTCAATCCCTTGTGTTTAAATTTGGCCATATAACGGAGATTAGAGAAAGATGATGT 133
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RESULT 10

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US-09-685-166A-536
; Sequence 536, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

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; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-685-166A-536

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Query Match 95.5%; Score 3797.8; DB 4; Length 6140;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 11

US-09-679-426-536  
; Sequence 536, Application US/09679426  
; Patent No. 6759515  
; GENERAL INFORMATION:

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
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; OTHER INFORMATION: n=A,T,C or G
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; Sequence 536, Application US/09759143  
; Patent No. 6800746  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 536  
; LENGTH: 6140  
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US-09-759-143-536  
Query Match 95.5%; Score 3797.8; DB 4; Length 6140;  
Best Local Similarity 99.9%; Pred. No. 0;  
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US-09-651-236-536  
; Sequence 536 Application US/09651236  
; Patent No. 6818751  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42718C18  
; CURRENT APPLICATION NUMBER: US/09/651,236  
; CURRENT FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 865  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 536  
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; OTHER INFORMATION: n=A,T,C or G  
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Qy 2234 TAAATGTCAGTGAATGAGAGGGAATGTAAACCGAGAAAGCTAGATCTTAACTGGTACT 2293  
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Qy 2294 TAGGAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGCATAGCAAGATCTCTAT 2353  
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Qy 2354 TGGTATTTCTACGCTCTTGTTTAACTCTTTCACAAACTTTTGCAACAAATGTTTGAAGTCAA 2413  
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Db 3833 ACTGCACCGTGTAAACCAATTTGCACACAGATTTGAACACCATTTATGACAGGACAAAGATA 3892
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Db 4013 CTGAAACAGCAAAACAGAT 4033

RESULT 14
US-09-636-215-824
; Sequence 824, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42171C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-215-824

Query Match 26.3%; Score 1047; DB 4; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 TCAGCCATTGAGAGGGTGTTCAGAGGCAATCGTCAGCATCCGAAAGATCCAGACCTTTTG 63
Qy 1171 CTACTTGTATGAGATATCAGAGGCAACCGTCAGTCGCGTCAGATGTTAAAAAGATGGTG 1230
Db 64 CTACTTGTATGAGATATCAGAGGCAACCGTCAGTCGCGTCAGATGTTAAAAAGATGGTG 123
Qy 1231 CATGTGCAGGATTTTACTGCTTTTGGGATAAGGCATCAGAGACCCCACTCTCAAGAGC 1290
Db 124 CATGTGCAGGATTTTACTGCTTTTGGGATAAGGCATCAGAGACCCCACTCTCAAGAGC 183
Qy 1291 CTTTTCCTTTACTGTCTCAGACCTGGCGAATTTAGTGTGTGTCGCGCCCGTGGGAGCAGGG 1350
Db 184 CTTTTCCTTTACTGTCTCAGACCTGGCGAATTTAGTGTGTGTCGCGCCCGTGGGAGCAGGG 243

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1531 TGTGCTCTGAAAGAAATTTACAGCTGTGTGGAGATGTTGATCTGACTGTGATAGGAGAT 1590
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664 ACTCATCAGTTGCAAGTACCTCAAGCTGCAAGTGCAGATTTCTGATATTCGAAAGATGTTAA 723
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; Sequence 824, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.

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; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-824

Query Match      26.3%; Score 1047; DB 4; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1171 CTACTTGTATGAGATATCACAGCGCAACCGTCAGCTGCGCTCAGATGTTAAAAGATGGTG 1230
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Qy 1591 CGGGGAACACGCTGAGTGGAGGGGAGAAAGCAAGGTAACCTTGCAGAGCAGTGTAT 1650
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Qy 1651 CAAGATGCTGACATCTATCTCTCGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGC 1710
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Job time : 632 secs



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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0

Maximum DB seq length: 500

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	216	5.4	291	US-09-636-215-823	Sequence 823, App
3	216	5.4	291	US-09-685-166A-823	Sequence 823, App
4	216	5.4	291	US-09-679-426-823	Sequence 823, App
5	216	5.4	291	US-09-759-143-823	Sequence 823, App
6	216	5.4	291	US-09-651-236-823	Sequence 823, App
7	28	0.7	34	US-09-636-215-831	Sequence 831, App
8	28	0.7	34	US-09-685-166A-831	Sequence 831, App
9	28	0.7	34	US-09-679-426-831	Sequence 831, App
10	28	0.7	34	US-09-759-143-831	Sequence 831, App
11	28	0.7	34	US-09-651-236-831	Sequence 831, App
12	28	0.6	35	US-09-636-215-828	Sequence 828, App
13	24	0.6	35	US-09-685-166A-828	Sequence 828, App
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18	24	0.6	36	US-09-685-166A-820	Sequence 820, App
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20	24	0.6	36	US-09-759-143-820	Sequence 820, App
21	24	0.6	36	US-09-651-236-820	Sequence 820, App
22	24	0.6	38	US-09-636-215-830	Sequence 830, App
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26	24	0.6	38	US-09-651-236-830	Sequence 830, App
27	21	0.5	340	US-09-281-646B-15	Sequence 15, Appl

28	19	0.5	19	4	US-09-281-646B-5	Sequence 5, Appli
c 29	19	0.5	418	4	US-09-621-976-17084	Sequence 17084, A
c 30	19	0.5	453	4	US-09-909-595-13	Sequence 13, Appl
c 31	18	0.5	18	4	US-09-281-646B-6	Sequence 6, Appli
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c 33	18	0.5	340	4	US-10-012-282-8	Sequence 8, Appli
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c 37	17	0.4	20	4	US-09-198-452A-2200	Sequence 2200, Ap
c 38	17	0.4	25	4	US-09-396-196G-93740	Sequence 93740, A
c 39	17	0.4	35	3	US-09-333-611-5	Sequence 5, Appli
c 40	17	0.4	64	4	US-09-513-999C-22958	Sequence 22958, A
c 41	17	0.4	143	4	US-09-513-999C-34244	Sequence 34244, A
c 42	17	0.4	176	4	US-09-513-999C-19865	Sequence 19865, A
c 43	17	0.4	216	4	US-09-107-433-1965	Sequence 1965, Ap
c 44	17	0.4	246	4	US-09-543-681A-3465	Sequence 3465, Ap
c 45	17	0.4	261	4	US-08-956-171E-2654	Sequence 2654, Ap

ALIGNMENTS

RESULT 1  
US-09-281-646B-28  
; Sequence 28, Application US/09281646B  
; Patent No. 6759238  
; GENERAL INFORMATION:  
; APPLICANT: Schuetz, John  
; APPLICANT: Friedland, Arnold  
; TITLE OF INVENTION: MULTIDRUG RESISTANCE ASSOCIATED PROTEINS AND USES THEREOF  
; FILE REFERENCE: SJ-0020  
; CURRENT APPLICATION NUMBER: US/09/281.646B  
; CURRENT FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 28  
; LENGTH: 443  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-281-646B-28

Query Match	6.5%;	Score 260;	DB 4;	Length 443;
Best Local Similarity	100.0%;	Pred. No. 1.4e-119;		
Matches 260;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	61	TTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCGAG	120	
Qy	3839	AAGCGCTGCGCTCACTGAAACAGCAAAACAGGATATCTTCAAAAGAAATTTATCCACATA	3898	
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RESULT 2  
US-09-636-215-823  
; Sequence 823, Application US/09636215  
; Patent No. 6620922  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.42717C17  
CURRENT APPLICATION NUMBER: US/09/636,215  
CURRENT FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 852  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 823  
LENGTH: 291  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-636-215-823

Query Match 5.4%; Score 216; DB 4; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3655 ATCCGGAGAAATTTGCCCACTGACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714  
Db 7 ATCCGGAGAAATTTGCCCACTGACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66  
Qy 3715 ATTGACAGCGCAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 3774  
Db 67 ATTGACAGCGCAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 126  
Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAAAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAAAGATGGTGCAACAACTGGGCAAG 186  
Qy 3835 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 222

RESULT 3  
US-09-685-166A-823  
Sequence 823, Application US/09685166A  
Patent No. 6630305  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C21  
CURRENT APPLICATION NUMBER: US/09/685,166A  
CURRENT FILING DATE: 2000-10-10  
NUMBER OF SEQ ID NOS: 898  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 823  
LENGTH: 291  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-685-166A-823

Query Match 5.4%; Score 216; DB 4; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3655 ATCCGGAGAAATTTGCCCACTGACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714  
Db 7 ATCCGGAGAAATTTGCCCACTGACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66  
Qy 3715 ATTGACAGCGCAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 3774  
Db 67 ATTGACAGCGCAAGATAATGGTTTATAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 126  
Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAAAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAAAGATGGTGCAACAACTGGGCAAG 186  
Qy 3835 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 222

RESULT 4  
US-09-679-426-823  
Sequence 823, Application US/09679426  
Patent No. 6759515  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C20  
CURRENT APPLICATION NUMBER: US/09/679,426  
CURRENT FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 895  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 823  
LENGTH: 291  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-679-426-823

Query Match 5.4%; Score 216; DB 4; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3655 ATCCGGAGAAATTTGCCCACTGACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714

Db 7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66  
Qy 3715 ATTGACAGCGACAAGATAATGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCGG 3774  
Db 67 ATTGACAGCGACAAGATAATGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCGG 126  
Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186  
Qy 3835 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 222

## RESULT 5

US-09-759-143-823

; Sequence 823, Application US/09759143

; Patent No. 6800746

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427223

; CURRENT APPLICATION NUMBER: US/09/759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 823

; LENGTH: 291

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-759-143-823

Query Match 5.4%; Score 216; DB 4; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3655 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714  
Db 7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66  
Qy 3715 ATTGACAGCGACAAGATAATGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCGG 3774  
Db 67 ATTGACAGCGACAAGATAATGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCGG 126  
Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186  
Qy 3835 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 222

## RESULT 6

US-09-651-236-823  
; Sequence 823, Application US/09651236  
; Patent No. 6818751  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.42718C18  
; CURRENT APPLICATION NUMBER: US/09/651,236  
; CURRENT FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 865  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 823  
; LENGTH: 291  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-651-236-823

Query Match 5.4%; Score 216; DB 4; Length 291;

Best Local Similarity 100.0%; Pred. No. 1.6e-97;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714  
Db 7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66  
Qy 3715 ATTGACAGCGACAAGATAATGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCGG 3774  
Db 67 ATTGACAGCGACAAGATAATGTTTATAGATTTCAGGAAGACTGGAAGAATATGATGAGCGG 126  
Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCCCTATTTTACAAGATGGTGCAACAACTGGGCAAG 186  
Qy 3835 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCGCTGCCCTCACTGAAACAGCAAAACAG 222

## RESULT 7

US-09-636-215-831/c

; Sequence 831, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

```
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 831
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-636-215-831
```

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Query Match 0.7%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2130 CTGGATTGCTTCATTTTCCTTATTC 2157
Db 34 CTGGATTGCTTCATTTTCCTTATTC 7
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```
RESULT 8
US-09-685-166A-831/c
; Sequence 831, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 831
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-685-166A-831
```

```
Query Match 0.7%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2130 CTGGATTGCTTCATTTTCCTTATTC 2157
Db 34 CTGGATTGCTTCATTTTCCTTATTC 7
```

```
RESULT 9
US-09-679-426-831/c
; Sequence 831, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 831
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-679-426-831
```

```
Query Match 0.7%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2130 CTGGATTGCTTCATTTTCCTTATTC 2157
Db 34 CTGGATTGCTTCATTTTCCTTATTC 7
```

```
RESULT 10
US-09-759-143-831/c
; Sequence 831, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
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; CURRENT FILING DATE: 2001-01-12  
 ; NUMBER OF SEQ ID NOS: 934  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 831  
 ; LENGTH: 34  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: PCR primer  
 US-09-759-143-831

Query Match 0.7%; Score 28; DB 4; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2130 CTGATTGTCCTTCATTTTCCTTATTC 2157  
 Db 34 CTGATTGTCCTTCATTTTCCTTATTC 7

RESULT 11  
 US-09-651-236-831/c  
 ; Sequence 831, Application US/09651236  
 ; Patent No. 6818751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.42718C18  
 ; CURRENT APPLICATION NUMBER: US/09/651,236  
 ; CURRENT FILING DATE: 2000-08-29  
 ; NUMBER OF SEQ ID NOS: 865  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 831  
 ; LENGTH: 34  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: PCR primer  
 US-09-651-236-831

Query Match 0.7%; Score 28; DB 4; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2130 CTGATTGTCCTTCATTTTCCTTATTC 2157  
 Db 34 CTGATTGTCCTTCATTTTCCTTATTC 7

RESULT 12  
 US-09-636-215-828  
 ; Sequence 828, Application US/09636215  
 ; Patent No. 6620922  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.42717C17  
 ; CURRENT APPLICATION NUMBER: US/09/636,215  
 ; CURRENT FILING DATE: 2000-08-10  
 ; NUMBER OF SEQ ID NOS: 852  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 828  
 ; LENGTH: 35  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: PCR primer  
 US-09-636-215-828

Query Match 0.6%; Score 24; DB 4; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAAATTTGCCCACTGC 3678  
 Db 12 ATCCGGAGAAATTTGCCCACTGC 35

RESULT 13  
 US-09-685-166A-828  
 ; Sequence 828, Application US/09685166A  
 ; Patent No. 6630305  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; FILE REFERENCE: 210121.427C21  
 ; CURRENT APPLICATION NUMBER: US/09/685,166A  
 ; CURRENT FILING DATE: 2000-10-10  
 ; NUMBER OF SEQ ID NOS: 898  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 828  
 ; LENGTH: 35  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:

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; OTHER INFORMATION: PCR primer
US-09-685-166A-828

Query Match      0.6%; Score 24; DB 4; Length 35;
Best Local Similarity 100.0%; Pred.No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCCACTGC 3678
Db 12 ATCCGGGAGAAATTTGCCCACTGC 35

RESULT 14
US-09-679-426-828
; Sequence 828, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121-427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 828
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-679-426-828

Query Match      0.6%; Score 24; DB 4; Length 35;
Best Local Similarity 100.0%; Pred.No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCCACTGC 3678
Db 12 ATCCGGGAGAAATTTGCCCACTGC 35

RESULT 15
US-09-759-143-828
; Sequence 828, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
```

```
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121-427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 828
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-759-143-828

Query Match      0.6%; Score 24; DB 4; Length 35;
Best Local Similarity 100.0%; Pred.No. 0.24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCCACTGC 3678
Db 12 ATCCGGGAGAAATTTGCCCACTGC 35

Search completed: May 20, 2005, 03:57:15
Job time : 621 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 23:49:26 ; Search time 16742 Seconds  
(without alignments)  
11513.251 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcgcgtgtaccagga.....ttttcgagacgactgtga 3978

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3974.8	99.9	4004	9 AY207008	AY207008 Homo sapi
2	3973.2	99.9	4231	6 AX210645	AX210645 Sequence
3	3973.2	99.9	4231	6 AX686744	AX686744 Sequence
4	3973.2	99.9	4231	9 AF071202	AF071202 Homo sapi
5	3968.4	99.8	5759	9 AF081219	AF081219 Homo sapi
6	3966	99.7	6082	6 AR278592	AR278592 Sequence
7	3966	99.7	6082	6 AR367288	AR367288 Sequence
8	3966	99.7	6082	6 AR400324	AR400324 Sequence
9	3966	99.7	6082	6 AR405591	AR405591 Sequence
10	3966	99.7	6082	6 AR563971	AR563971 Sequence
11	3966	99.7	6082	6 AX141045	AX141045 Sequence
12	3966	99.7	6082	6 AX200905	AX200905 Sequence
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15	3965.4	99.7	4515	6 CQ490536	CQ490536 Sequence
16	3965.4	99.7	4515	6 CQ492310	CQ492310 Sequence
17	3965.4	99.7	4515	6 CQ492702	CQ492702 Sequence
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19	3965.4	99.7	4515	6 CQ496370	CQ496370 Sequence

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21	3797.8	95.5	6140	6 AR367289	AR367289 Sequence
22	3797.8	95.5	6140	6 AR400325	AR400325 Sequence
23	3797.8	95.5	6140	6 AR405592	AR405592 Sequence
24	3797.8	95.5	6140	6 AR563972	AR563972 Sequence
25	3797.8	95.5	6140	6 AX141046	AX141046 Sequence
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27	3797.8	95.5	6140	6 AX267562	AX267562 Sequence
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29	2818	70.8	4526	10 AY533524	AY533524 Rattus no
30	2733.8	68.7	2940	9 AF071203	AF071203 Homo sapi
31	2716.6	68.3	3372	6 CQ725032	CQ725032 Sequence
32	2669.2	67.1	4415	10 AY533525	AY533525 Rattus no
33	2537.8	63.8	2890	9 BC041560	BC041560 Homo sapi
34	2480.2	62.3	4299	9 HSM807262	HSM807262 Homo sapi
35	2323.6	58.4	4878	5 AJ719382	AJ719382 Gallus ga
36	1893.2	47.6	2103	9 AY133680	AY133680 Homo sapi
37	1892.8	47.6	2143	9 AY133678	AY133678 Homo sapi
38	1892.8	47.6	2256	9 AY133679	AY133679 Homo sapi
39	1047	26.3	1074	6 AR400537	AR400537 Sequence
40	1047	26.3	1074	6 AR405804	AR405804 Sequence
41	1047	26.3	1074	6 AR564184	AR564184 Sequence
42	1047	26.3	1074	6 AX201051	AX201051 Sequence
43	1047	26.3	1074	6 AX267850	AX267850 Sequence
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45	707.4	17.8	768	6 CQ480961	CQ480961 Sequence

## ALIGNMENTS

RESULT 1  
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LOCUS Homo sapiens ATP-binding cassette transporter C4 (ABCC4) mRNA,  
DEFINITION complete cds.  
ACCESSION AY207008  
VERSION AY207008.1 GI:31322320  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 4004)  
Kato,R. and Ishikawa,T.  
AUTHORS Direct Submission  
TITLE Submitted (24-DEC-2002) Department of Biomolecular Engineering,  
JOURNAL Graduate School of Bioscience and Biotechnology, Tokyo Institute of  
Technology, 4259 Nagatsuda-cho, Midori-ku, Yokohama-shi, Kanagawa  
226-8501, Japan  
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FETAL"

ORIGIN

Query Match	99.9%;	Score	3974.8;	DB	9;	Length	4004;		
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Qy	181	CAAGGGTCTGGGATAAGAAGTTTTAAGAGCTGAGAATACGCACAGAGAAGCTTCTTTA	240						
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Db	246	ACAAGACATCATAAAGTGTACTGGAATCTTATTAGTTTGGGAAATTTTACGTTA	305						
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LOCUS AX210645 4231 bp DNA linear PAT 31-AUG-2001  
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 Metagen Gesellschatt fuer Genomforschung mbH (DE)  
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Eulenbergh, K., Broenner, G., Ciossek, T., Haeder, T. and Steuernagel, A.  
Protein disulfide isomerase and ABC transporter homologous proteins  
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Patent: WO 02079238-A 3 10-OCT-2002;  
JOURNAL  
Develogen Aktiengesellschaft fuer Entwicklungsbiologische Forschung  
(DE)

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VERSION	AF071202.1 GI:3335172		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
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AUTHORS	Lee, K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.		
TITLE	Isolation of MOAT-B, a widely expressed multidrug resistance-associated protein/canalicular multispecific organic anion transporter-related transporter		
JOURNAL	Cancer Res. 58 (13), 2741-2747 (1998)		
MEDLINE	98324262		
PUBMED	9661885		
REFERENCE	2 (bases 1 to 4231)		
AUTHORS	Lee, K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-JUN-1998) Medical Oncology, Fox Chase Cancer Center, 7701 Burholme Ave., Philadelphia, PA 19111, USA		
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ORIGIN

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LOCUS  
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ACCESSION AY081219  
VERSION AY081219.1 GI:21655122  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 5759)  
AUTHORS Adachi,M., Sampath,J., Lan,L.B., Sun,D., Hargrove,P., Flatley,R., Tatum,A., Edwards,M.Z., Wezeman,M., Matherly,L., Drake,R. and Schuetz,J.  
TITLE Expression of MRP4 Confers Resistance to Ganciclovir and Compromises Bystander Cell Killing  
J. Biol. Chem. 277 (41), 38998-39004 (2002)  
12105214  
JOURNAL  
PUBMED 2 (bases 1 to 5759)  
AUTHORS Adachi,M., Sampath,J., Sun,D. and Schuetz,J.D.  
TITLE Direct Submission  
JOURNAL Submitted (22-FEB-2002) Pharmaceutical Sciences, St. Jude Children's Research Hospital, 332 North Lauderdale St., Memphis, TN 38105-2794, USA  
FEATURES  
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KEYWORDS	Unknown.		
SOURCE	Unknown.		
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UNCLASSIFIED	Unclassified.		

REFERENCE	1	(bases 1 to 6082)	
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: US 6512094-A 535 28-JAN-2003;		
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Best Local Similarity	100.0%; Pred. No. 0;		
Matches 3977; Conservative	0; Mismatches 0; Indels 1; Gaps 1;		
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RESULT 7  
 AR367288  
 LOCUS  
 DEFINITION Sequence 535 from patent US 6329505.  
 ACCESSION AR367288  
 linear PAT 12-SEP-2003

VERSION AR367288.1 GI:34600263  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 6082)  
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J., Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and Day,C.H.  
 TITLE Compositions and methods for therapy and diagnosis of prostate cancer  
 JOURNAL Patent: US 6329505-A 535 11-DEC-2001;  
 FEATURES Location/Qualifiers  
 source 1..6082  
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 ORIGIN  
 Query Match 99.7%; Score 3966; DB 6; Length 6082;  
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DEFINITION Sequence 535 from patent US 6620922.  
ACCESSION AR400324  
VERSION AR400324.1 GI:40143590  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6082)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,  
Kalos,M.D., Fanger,G.R., Retter,W., Stolk,J.A., Day,C.H.,  
Vedick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,  
Hepler,W.T. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: US 6620922-A 535 16-SEP-2003;  
FEATURES Location/Qualifiers  
source 1..6082  
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ORIGIN  
Query Match 99.7%; Score 3966; DB 6; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 397; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 ATGCTGCCGTACACAGGAGTGAAGCCCAACCGCTGCGAGGACGGAACCTCTGCTCA 60  
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ACCESSION AR405591  
VERSION AR405591.1 GI:40154428  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6082)  
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T. and Henderson, R. A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6630305-A 535 07-OCT-2003;  
FEATURES  
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/organism="unknown"  
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ORIGIN

Query Match 99.7%; Score 3966; DB 6; Length 6082;  
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Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DEFINITION AR563971  
ACCESSION AR563971  
VERSION AR563971.1 GI:53979022  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6082)  
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.F. and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer  
JOURNAL Patent: US 6759515-A 535 06-JUL-2004;  
FEATURES Location/Qualifiers  
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Query Match 99.7%; Score 3966; DB 6; Length 6082;  
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Db 366 CAAGGTTCTGGGATAAAGATTTTAAAGCTGAGATGACGACAGAGCCCTTCTTTTA 425

Qy 241 ACAAGACAATCATAAAGTGTACTGGAAATCTTATTAGTTTGGGAAATTTTACGTTA 300  
Db 426 ACAAGACAATCATAAAGTGTACTGGAAATCTTATTAGTTTGGGAAATTTTACGTTA 485

Qy 301 ATTGAGGAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAAATTAATTAATTTT 360  
Db 486 ATTGAGGAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAAATTAATTAATTTT 545

Qy 361 GAAATTTATGATCCCATGATTTCTGTGGCTTTTGAACACAGCGGTACGCTATGCCACCGTG 420  
Db 546 GAAATTTATGATCCCATGATTTCTGTGGCTTTTGAACACAGCGGTACGCTATGCCACCGTG 605

Qy 421 CTGACTTTTTCACGCTCATTTTGGCTATACGTCACTATATTTTATTTTATCAGTTTCA 480  
Db 606 CTGACTTTTTCACGCTCATTTTGGCTATACGTCACTATATTTTATTTTATCAGTTTCA 665

Qy 481 TGTCTGGGATGAGTTACGATGAGCCATGTGCCATATGATTTTATCGGAGGCACTTCGT 540  
Db 666 TGTCTGGGATGAGTTACGATGAGCCATGTGCCATATGATTTTATCGGAGGCACTTCGT 725

Qy 541 CTTAGTAAACATGGCCATGGGGAAGACAAACACAGCCAGATAGTCAATCTCTGTCTCAAT 600  
Db 726 CTTAGTAAACATGGCCATGGGGAAGACAAACACAGCCAGATAGTCAATCTCTGTCTCAAT 785

Qy 601 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGTGGGAGGACCACTG 660  
Db 786 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGTGGGAGGACCACTG 845

Qy 661 CAGCGCATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGTCTGTCTGGG 720  
Db 846 CAGCGCATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGTCTGTCTGGG 905

Qy 721 ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAGAGCTGTGTTTGGGAAGTGTGTTCTCATCA 780  
Db 906 ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAGAGCTGTGTTTGGGAAGTGTGTTCTCATCA 965

Qy 781 CTGAGGAGTAAACTGCAACTTTTTCACCGATGCCAGGATCAGGACCATGAATGAATTTATA 840  
Db 966 CTGAGGAGTAAACTGCAACTTTTTCACCGATGCCAGGATCAGGACCATGAATGAATTTATA 1025

Qy 841 ACTGCTATAAGGATAATAAATAATGTCGCTGGGAAAGTCAATTTTCAAACTTTATTATACC 900  
Db 1026 ACTGCTATAAGGATAATAAATAATGTCGCTGGGAAAGTCAATTTTCAAACTTTATTATACC 1085

Qy 901 AATTGAGAAGAGGAGATTTCAGAGATTCTGAGAAAGTTCCTGCTCAGGGGGATGAAT 960  
Db 1086 AATTGAGAAGAGGAGATTTCAGAGATTCTGAGAAAGTTCCTGCTCAGGGGGATGAAT 1145

Qy 961 TTGGCTTCGTTTTCAGTGCAGCAAAATCATCTGTGTTGTGACCTTCACCACCTACGTCG 1020  
Db 1146 TTGGCTTCGTTTTCAGTGCAGCAAAATCATCTGTGTTGTGACCTTCACCACCTACGTCG 1205

Qy 1021 CTCCTCGGCAGTGTGATCACAGCCAGCCGCTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080  
Db 1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy 1081 GTGCGGCTGACGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTTCAGAGGCAATC 1140  
Db 1266 GTGCGGCTGACGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTTCAGAGGCAATC 1325

Qy 1141 GTCAGCATCGAGAAATCCAGACCTTTTGTCTACTTGTATGAGATATCACAGCGCAACCGT 1200  
Db 1326 GTCAGCATCGAGAAATCCAGACCTTTTGTCTACTTGTATGAGATATCACAGCGCAACCGT 1385

Qy 1201 CAGCTGCCCTCAGATGTTAAAGATGCTGATGCGAGGATTTTACTGCTTTTGGGAT 1260  
Db 1386 CAGCTGCCCTCAGATGTTAAAGATGCTGATGCGAGGATTTTACTGCTTTTGGGAT 1445

Qy 1261 AAGSCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTACTGTGACAGCTGGCGAATTTG 1320  
Db 1446 AAGSCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTACTGTGACAGCTGGCGAATTTG 1505

Qy 1321 TTAGCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCACTGTTTAAGTCCGCTGCTCGGG 1380  
Db 1506 TTAGCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCACTGTTTAAGTCCGCTGCTCGGG 1565

Qy 1381 GAATTGSCCCCAAGTCAAGGCTGTGATGCGATGCAAGAAATTTGCTATGTGCTCAG 1440  
Db 1566 GAATTGSCCCCAAGTCAAGGCTGTGATGCGATGCAAGAAATTTGCTATGTGCTCAG 1625

Qy 1441 CAGCCCTGGGTGTTTCTCGGAACTCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
Db 1626 CAGCCCTGGGTGTTTCTCGGAACTCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy 1501 AAGGAACGATATGAATAAGTCAATAAGGCTTGTCTCTGAAAAAGGATTTTACAGCTGTTG 1560  
Db 1686 AAGGAACGATATGAATAAGTCAATAAGGCTTGTCTCTGAAAAAGGATTTTACAGCTGTTG 1745

Qy 1561 GAGGATGCTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA 1620  
Db 1746 GAGGATGCTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA 1805

Qy 1621 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGGACGAT 1680

Db	1806	GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGCGAGAT	1865
Qy	1681	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACATGTTGCGAATCTGTGTATTTGCAA	1740
Db	1866	CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACATGTTGCGAATCTGTGTATTTGCAA	1925
Qy	1741	ATTTTGCATGAGAGATCACAAATTTTATGACTCATCAGTGTGAGTACCTCAAGACTGCA	1800
Db	1926	ATTTTGCATGAGAGATCACAAATTTTATGACTCATCAGTGTGAGTACCTCAAGACTGCA	1985
Qy	1801	AGTCAGATTTCTGATATTGAAGAATGGTAAATGCTGAGAGGGGCACTTACACTGAGTTC	1860
Db	1986	AGTCAGATTTCTGATATTGAAGAATGGTAAATGCTGAGAGGGGCACTTACACTGAGTTC	2045
Qy	1861	CTAAAACTCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATTAATGAGGAAAGTGAACAA	1920
Db	2046	CTAAAACTCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATTAATGAGGAAAGTGAACAA	2105
Qy	1921	CCTCCAGTTCGAGGAACTCCACACACTAAGGATCGTACCTTCTCAGAGTCTTCGCGTTGG	1980
Db	2106	CCTCCAGTTCGAGGAACTCCACACACTAAGGATCGTACCTTCTCAGAGTCTTCGCGTTGG	2165
Qy	1981	TCTCAACAACTCTTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAGAGATACAGAG	2040
Db	2166	TCTCAACAACTCTTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAGAGATACAGAG	2225
Qy	2041	AATGTCGAGTTACACTATACAGAGGAGAACCGTTTCTGAAGAAAGTTGGTTTTCAGGCC	2100
Db	2226	AATGTCGAGTTACACTATACAGAGGAGAACCGTTTCTGAAGAAAGTTGGTTTTCAGGCC	2285
Qy	2101	TATAAGAAATTAATTCAGAGCTGGTGTCTCAGTGGATGCTCTCATTTTCCCTATTTCTCCTA	2160
Db	2286	TATAAGAAATTAATTCAGAGCTGGTGTCTCAGTGGATGCTCTCATTTTCCCTATTTCTCCTA	2345
Qy	2161	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTCATCTCGGCGAAAC	2220
Db	2346	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTCATCTCGGCGAAAC	2405
Qy	2221	AAACAAAGTATGCTAAATGTCACTGTAAATGAGGAGGAGAAATGTAACCGAGAAGCTAGAT	2280
Db	2406	AAACAAAGTATGCTAAATGTCACTGTAAATGAGGAGGAGAAATGTAACCGAGAAGCTAGAT	2465
Qy	2281	CTTTAACTGGTACTTAAAGAAATTTATTCAGGTTTAACTGTAGCTACGGTCTTTTGGCATA	2340
Db	2466	CTTTAACTGGTACTTAAAGAAATTTATTCAGGTTTAACTGTAGCTACGGTCTTTTGGCATA	2525
Qy	2341	GCAAGATCTCTATTGGTATTCTACGTCTCTGTTAACTCTTCAACAACTTTGCAACAAACAA	2400
Db	2526	GCAAGATCTCTATTGGTATTCTACGTCTCTGTTAACTCTTCAACAACTTTGCAACAAACAA	2585
Qy	2401	ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTTATTTCTTTGATGAAATTTCCAAATAGGAAGA	2460
Db	2586	ATGTTTGAGTCAATTTCTGAAAGCTCCGGTATTTATTTCTTTGATGAAATTTCCAAATAGGAAGA	2645
Qy	2461	ATTTTAAATCGTTTCTCCAAAGACATTTGACATTTGGATGATTTGCTGCGCTCAGCTTTT	2520
Db	2646	ATTTTAAATCGTTTCTCCAAAGACATTTGACATTTGGATGATTTGCTGCGCTCAGCTTTT	2705
Qy	2521	TTAGATTTTCATCCAGACATTTGCTACAGTGGTGGTGGTGGTCTCTGTGGCTGTGGCCCGTG	2580
Db	2706	TTAGATTTTCATCCAGACATTTGCTACAGTGGTGGTGGTGGTCTCTGTGGCTGTGGCCCGTG	2765
Qy	2581	ATTCTTTGGATTCGCAATACCTTCGTTCCCTTGGATTCATTTTTCATTTTCTTCGCGGA	2640
Db	2766	ATTCTTTGGATTCGCAATACCTTCGTTCCCTTGGATTCATTTTTCATTTTCTTCGCGGA	2825
Qy	2641	TATTTTGTGAAACGTCAGAGATCTGAAGCGCTGGAACTCAACACTCGGAGTCCAGTG	2700
Db	2826	TATTTTGTGAAACGTCAGAGATCTGAAGCGCTGGAACTCAACACTCGGAGTCCAGTG	2885
Qy	2701	TTTTCACACTTGTCTATCTTCTCTCAGGGGCTCTGGACCATCCGCGCATACAAAGCAGAA	2760

Db	2886	TTTTCCCACTTGTCTATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2945
Qy	2761	GAGAGGTGTGAGGAACTGTTTGTATGACACACAGAGATTTTACATTCAGAGGCTTGGTTCTTG	2820
Db	2946	GAGAGGTGTGAGGAACTGTTTGTATGACACACAGAGATTTTACATTCAGAGGCTTGGTTCTTG	3005
Qy	2821	TTTTTGACAAAGCTCCCGCTGTTGCGCGTCCGTCTGATGCGATCTCTGTCGCAATGTTGTC	2880
Db	3006	TTTTTGACAAAGCTCCCGCTGTTGCGCGTCCGTCTGATGCGATCTCTGTCGCAATGTTGTC	3065
Qy	2881	ATCATCTGTTGCCCTTTGGGTCCTGATTTCTGGCAAAAACTCTGGATGCGGGCAGGTTGGT	2940
Db	3066	ATCATCTGTTGCCCTTTGGGTCCTGATTTCTGGCAAAAACTCTGGATGCGGGCAGGTTGGT	3125
Qy	2941	TTGGCACTGCTCTATGCGCTCACGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3000
Db	3126	TTGGCACTGCTCTATGCGCTCACGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3185
Qy	3001	GCTGAAGTTCGAGAAATATGATGATCTCAGTAGAAGAGGTCTATTGAATACACAGACCTTGAA	3060
Db	3186	GCTGAAGTTCGAGAAATATGATGATCTCAGTAGAAGAGGTCTATTGAATACACAGACCTTGAA	3245
Qy	3061	AAAGAACACCTTTGGGHAATATCAGAAACGCCACACACAGCTGGCCCCATGAAAGGAGTG	3120
Db	3246	AAAGAACACCTTTGGGHAATATCAGAAACGCCACACACAGCTGGCCCCATGAAAGGAGTG	3305
Qy	3121	ATAATCTTTTACAAATGTAATCTCAGTCCAGTGGGCTCTGTTACTGTAACGAT	3180
Db	3306	ATAATCTTTTACAAATGTAATCTCAGTCCAGTGGGCTCTGTTACTGTAACGAT	3365
Qy	3181	CTGACACACTCATTTAAATCAAGAAAGAGTTGGCATTTGGGAAAGAACCGGAGCTGGA	3240
Db	3366	CTGACACACTCATTTAAATCAAGAAAGAGTTGGCATTTGGGAAAGAACCGGAGCTGGA	3425
Qy	3241	AAAAGTTCCCTCATCTCAGCCCTTTTATGATTTGTCAGAACCCGAGGTAATAATTTGGAT	3300
Db	3426	AAAAGTTCCCTCATCTCAGCCCTTTTATGATTTGTCAGAACCCGAGGTAATAATTTGGAT	3485
Qy	3301	GATGAATCTTGACAACTGAAATTTGGACTTCAAGATTTAAGGAAGAAATGTCATCATATA	3360
Db	3486	GATGAATCTTGACAACTGAAATTTGGACTTCAAGATTTAAGGAAGAAATGTCATCATATA	3545
Qy	3361	CCTCAGGAACTGTTTGTGTTTCACTGGAAACATGAGGAAACACCTGGATCCCTTTAATGAG	3420
Db	3546	CCTCAGGAACTGTTTGTGTTTCACTGGAAACATGAGGAAACACCTGGATCCCTTTAATGAG	3605
Qy	3421	CACACGGATGAGGAACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA	3480
Db	3606	CACACGGATGAGGAACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA	3665
Qy	3481	GATCTTCTGGTAAATGGATACCTGAATTTAGCAGAAATCAGGATCCAAATTTTGTGTTGGA	3540
Db	3666	GATCTTCTGGTAAATGGATACCTGAATTTAGCAGAAATCAGGATCCAAATTTTGTGTTGGA	3725
Qy	3541	CAAAAGCAACTGGTGTGCTTGGCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTTAT	3600
Db	3726	CAAAAGCAACTGGTGTGCTTGGCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTTAT	3785
Qy	3601	GATGAAGCGACGGCAATGTGGATCCCAAGAACTGATGAGTTTAAATACAAAAAAATCCGG	3660
Db	3786	GATGAAGCGACGGCAATGTGGATCCCAAGAACTGATGAGTTTAAATACAAAAAAATCCGG	3844
Qy	3661	GAGAAATTTGCCCACTGCACCGTCTAACCAATTCACACAGATTTGAAACCATTTATTGAC	3720
Db	3845	GAGAAATTTGCCCACTGCACCGTCTAACCAATTCACACAGATTTGAAACCATTTATTGAC	3904
Qy	3721	AGCCACAAGATAATGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGCTATGTT	3780
Db	3905	AGCCACAAGATAATGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGCTATGTT	3964
Qy	3781	TTGCTGCAAAATAAAGAGAGCTTATTTTAAAGATGTTGCAACAACTGGGGCAAGCAGAA	3840
Db	3965	TTGCTGCAAAATAAAGAGAGCTTATTTTAAAGATGTTGCAACAACTGGGGCAAGCAGAA	4024



Db 1686 AAGGAACGATATGAAAAAGTCATAAAGCGTTGTGCTCTGTAAGAAAGGATTTACAGCTGTG 1745  
Qy 1561 GAGGATGGTATCTGACTGTGATAGGAGATCGGGGAACCGCTGAGTGGGGCAGAAA 1620  
Db 1746 GAGGATGGTATCTGACTGTGATAGGAGATCGGGGAACCGCTGAGTGGGGCAGAAA 1805  
Qy 1621 GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1680  
Db 1806 GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1865  
Qy 1681 CCTCTCAGTGCAGTGTAGTGGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAA 1740  
Db 1866 CCTCTCAGTGCAGTGTAGTGGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAA 1925  
Qy 1741 ATTTTGCATGAGAAGATCACAATTTTGTAGTGAATCTCATCAGTTGCGAGTACCTCAAGAGCTGCA 1800  
Db 1926 ATTTTGCATGAGAAGATCACAATTTTGTAGTGAATCTCATCAGTTGCGAGTACCTCAAGAGCTGCA 1985  
Qy 1801 AGTCAGATTTCTGATATTGAAGATGGTAAATGGTGCAGAGGGGACTTTACACTGAGTTTC 1860  
Db 1986 AGTCAGATTTCTGATATTGAAGATGGTAAATGGTGCAGAGGGGACTTTACACTGAGTTTC 2045  
Qy 1861 CTAAAACTCTGTATAGATTTTGGCTCCCTTTTAAAGGAAGGATAATGAGGAAGTGAACAA 1920  
Db 2046 CTAAAACTCTGTATAGATTTTGGCTCCCTTTTAAAGGAAGGATAATGAGGAAGTGAACAA 2105  
Qy 1921 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980  
Db 2106 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165  
Qy 1981 TCTCAACAATCTTCTAGACCTCTCTGAAAGATGGTCTCGAGAGCCAGAGATACAGAG 2040  
Db 2166 TCTCAACAATCTTCTAGACCTCTCTGAAAGATGGTCTCGAGAGCCAGAGATACAGAG 2225  
Qy 2041 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTCAGGCC 2100  
Db 2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTCAGGCC 2285  
Qy 2101 TATAAGAAATTAATTCAGAGCTGGTGTCTCAGTGAATGTCTTCATTTTCCCTTATCTCCTA 2160  
Db 2286 TATAAGAAATTAATTCAGAGCTGGTGTCTCAGTGAATGTCTTCATTTTCCCTTATCTCCTA 2345  
Qy 2161 AACACTGCAGCTCAGTTGGCTGTATGTCTCAAGATTTGGTGGCTTCATCTCGGGCAAC 2220  
Db 2346 AACACTGCAGCTCAGTTGGCTGTATGTCTCAAGATTTGGTGGCTTCATCTCGGGCAAC 2405  
Qy 2221 AAACAAAGTATGCTAAATGTCACTGTATAATGAGGAGGAAATGTAAACCGAAGCTAGAT 2280  
Db 2406 AAACAAAGTATGCTAAATGTCACTGTATAATGAGGAGGAAATGTAAACCGAAGCTAGAT 2465  
Qy 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGGCATA 2340  
Db 2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTTCTTTTGGGCATA 2525  
Qy 2341 GCAAGATCTTATTTGGTATCTACGTCTCTGTAACTCTTCAACAACTTTGACACAA 2400  
Db 2526 GCAAGATCTTATTTGGTATCTACGTCTCTGTAACTCTTCAACAACTTTGACACAA 2585  
Qy 2401 ATGTTTGGATCAATTTCTGAAGCTCCGGTATTTATTTTGTATAGAAATCCAATAGGAAGA 2460  
Db 2586 ATGTTTGGATCAATTTCTGAAGCTCCGGTATTTATTTTGTATAGAAATCCAATAGGAAGA 2645  
Qy 2461 ATTTTAAATCGTTTCTCAAGACATTTGGACACTTTGGATGATTTGCTGCGCGCTGACGTTT 2520  
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Qy 2641 TATTTTGGAAACGTCAGAGATGTGAAGCGCTGGAATCTCAAACTCGSAGTCCAGTG 2700  
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Db 2886 TTTTCCCACTTGTCACTCTCTCTCCAGGGGCTCTGGAACCATCCGGGCATACAAAGCAGAA 2945  
Qy 2761 GAGAGTGTGAGGAACGTGTTTGTATGACACACAGGATTTACATTCAGAGGCTTGTCTTGT 2820  
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Qy 3181 CTGACACACTCATTAATCACAAGAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
Db 3366 CTGACACACTCATTAATCACAAGAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3425  
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Db 3845 GAGAAATTTGCCACTGCAACGCTGCTAACCAATTCGACACAGATTTGAACACCATTTATTCAC 3904







Qy 1441 CAGCCCTGGGTGTTCTCGGAACTCTCAGAGAGTAATATTTTATTTTGGGAAGAAATACGAA 1500  
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 Qy 1741 ATTTTGCATGAGAAAGATCACAAATTTTAGTGACTCATCAGTTGCGAGTACCTCAAAGCTGCA 1800  
 Db 1926 ATTTTGCATGAGAAAGATCACAAATTTTAGTGACTCATCAGTTGCGAGTACCTCAAAGCTGCA 1985  
 Qy 1801 AGTCAGATTTCTGATATTGAAAGATGGTAAATGTGTGCAAGAGGGGACTTACACTGAGTTC 1860  
 Db 1986 AGTCAGATTTCTGATATTGAAAGATGGTAAATGTGTGCAAGAGGGGACTTACACTGAGTTC 2045  
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 Db 2046 CTAAAACTCGTATAGATTTTGGCTCCCTTTTAAAGAGAGGATATGAGGAAAGTGAACAA 2105  
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 Db 2106 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGGTTGG 2165  
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 Qy 2161 AACACTGAGCTCAGGTTCCTATGTGCTTCAAGATTTGGTGGCTTTTATCTAGGGCAAC 2220  
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LOCUS Sequence 535 from Patent WO0173032.  
DEFINITION AX267561  
ACCESSION AX267561  
VERSION AX267561.1 GI:16516283  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,  
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,  
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.  
and Henderson,R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: WO 0173032-A 535 04-OCT-2001;  
CORIXA CORPORATION (US)  
FEATURES  
source 1. 6082  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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ORIGIN  
Query Match 99.7%; Score 3966; DB 6; Length 6082;  
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Qy	3901	GCTCAGCTGACCATGTTTACAAACACTTCCAAATGGACAGCGCTCGACCTTAACTATT	3960	Qy	541	CTTAGTAACATGGCCATGGGGAACACCAACAGCCAGATAGTCAATCTGCTGCCAAT	600
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KEYWORDS	Homo sapiens (human)			Db	879	CTGAGGATGATAAACTGCAACTTTTCAAGATGCGAGGATCAGGACCATGAATGAAGTTATA	938
ORGANISM	Homo sapiens			Qy	841	ACTGGTATAAGGATAATAAAATGTAAGCTGCGCTGGGAAAAGTCAATTTTCAAAATCTTAT	900
REFERENCE	Schlegel R., Endege W.O. and Monahan J.E.			Db	939	ACTGGTATAAGGATAATAAAATGTAAGCTGCGCTGGGAAAAGTCAATTTTCAAAATCTTAT	998
AUTHORS	Genes differentially expressed in human prostate cancer and their			Qy	901	AATTTGAGAAAGAGGAGATTTCCAAAGATTTCTGAGAGATTTCTGCTCAGGGGATGAAT	960
TITLE	use			Db	999	AATTTGAGAAAGAGGAGATTTCCAAAGATTTCTGAGAGATTTCTGCTCAGGGGATGAAT	1058
JOURNAL	Patent: WO 0160860-A 20660 23-AUG-2001;			Qy	961	TTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCTGTGTTGTGACCTTCAACACCTACCTG	1020
FEATURES	Millennium Predictive Medicine, Inc. (US)			Db	1059	TTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCTGTGTTGTGACCTTCAACACCTACCTG	1118
source	Location/Qualifiers			Qy	1021	CTCTCGGCAAGTGTGATCAGCGCGCGGTGTTCTGCGAGTGAGCGCTGTATGGGGCT	1080
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Query Match	99.7%; Score 3965.4; DB 6; Length 4515;			Qy	1081	GTGCGGCTGACGGTTACCTCTTCTCCCTCAGCCATTTGAGGGGTGTGAGAGCAATC	1140
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Matches 3977;	Conservative 0; Mismatches 1; Indels 1; Gaps 1;			Qy	1141	GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTGTAGATATACAGCGCAACCGT	1200
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Db	99	ATGCTGCCGTGTACCAAGAGGTGAAGCCAAACCGCTGCAAGGACGGAACCTCTGCTCA	158	Qy	1201	CAGCTGCCGTGAGATGTTAAAGAGATGGTGTGATGATGATGATGATGATGATGATGATG	1260
Qy	61	CGCGTGTCTTCTGCTGCTCAATCCCTGTTTAAATTTGGCCATAAACGGAGATTAG	120	Db			
Db	159	CGCGTGTCTTCTGCTGCTCAATCCCTGTTTAAATTTGGCCATAAACGGAGATTAG	218	Qy			
Qy	121	GAAGATGATATGTTTTCAGTGTCTGCCAGAGACCGCTCACAGCACCTTTGGAGAGGTTG	180				

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Qy	1501	AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTG	1560
Db	1599	AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTG	1658
Qy	1561	GAGGATGGTGATCTCACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGGCAGAAA	1620
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VERSION CQ490536.1 GI:41456155
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E.
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3219 GATAATCTTTGACAATGTGAACCTTATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCA 3278  
3180 TCTGACAGCACTCATTTAAATCAGAAAGGTTGGCATTTGTGGGAAGAACCGGAGCTGG 3239  
3279 TCTGACAGCACTCATTTAAATCAGAAAGGTTGGCATTTGTGGGAAGAACCGGAGCTGG 3338  
3240 AAAAAGTTCCCTCATCTCAGCCCTTTTATAGTTGTGAGAACCCCAAGGTAAAAATTTGGAT 3299  
3339 AAAAAGTTCCCTCATCTCAGCCCTTTTATAGTTGTGAGAACCCCAAGGTAAAAATTTGGAT 3398  
3300 TGATAAGATCTTGACAACTGAAATTTGACCTTACGATTTTAAAGGAAGAAATGTCAATCAT 3359  
3399 TGATAAGATCTTGACAACTGAAATTTGACCTTACGATTTTAAAGGAAGAAATGTCAATCAT 3458



Qy	3360	ACCTCAGGAACCTGTTTGTCTCACTGGAAACAATGAGGAAAAAACCCTGGATCCCTTTTAATGA	3419
Db	3459	ACCTCAGGAACCTGTTTGTCTCACTGGAAACAATGAGGAAAAAACCCTGGATCCCTTTTAATGA	3518
Qy	3420	GCACACGGATGAGGAACTGTGGAAATGCTTACAAGAGAGTCAACTTAAGAAACCAATTGA	3479
Db	3519	GCACACGGATGAGGAACTGTGGAAATGCTTACAAGAGAGTCAACTTAAGAAACCAATTGA	3578
Qy	3480	AGATCTTCTGGTAAAAATGGATACTGAATTAGCGAATCAGGATCCAAATTTTAGTGTGG	3539
Db	3579	AGATCTTCTGGTAAAAATGGATACTGAATTAGCGAATCAGGATCCAAATTTTAGTGTGG	3638
Qy	3540	ACAAGACAACTGGTGTGCCCTTCCGAGGCAATTTCTCAGGAAAAATCAGATATTGATTAT	3599
Db	3639	ACAAGACAACTGGTGTGCCCTTCCGAGGCAATTTCTCAGGAAAAATCAGATATTGATTAT	3698
Qy	3600	TGATGAAGCGACGGCAAAATGGGATCCAAGAACTGATGAGTTAATCAAAAAAAAATCCG	3659
Db	3699	TGATGAAGCGACGGCAAAATGGGATCCAAGAACTGATGAGTTAATCAAAAAAAAATCCG	3758
Qy	3660	GGAGAAATTTTGCCCACTGCACCGTGCTAAACAATTGCACA CAGATTTGAACAACCAATTATGA	3719
Db	3759	GGAGAAATTTTGCCCACTGCACCGTGCTAAACAATTGCACA CAGATTTGAACAACCAATTATGA	3818
Qy	3720	CAGCGACAAGATAATGCTTTTAGATTTCAGAGAGACTGAAAGAAATATGATCAGCCGTATGT	3779
Db	3819	CAGCGACAAGATAATGCTTTTAGATTTCAGAGAGACTGAAAGAAATATGATCAGCCGTATGT	3878
Qy	3780	TTTGCTGCAAAAATAAGAGAGCCCTATTTTACAAGATGGTCAACAACCTGGGCAAGGCAGA	3839
Db	3879	TTTGCTGCAAAAATAAGAGAGCCCTATTTTACAAGATGGTCAACAACCTGGGCAAGGCAGA	3938
Qy	3840	AGCCGCTGCCCTCACTGAAAACAGCAAAACAGGTATTAATTTCAAAGAAATTTATCCACATAT	3899
Db	3939	AGCCGCTGCCCTCACTGAAAACAGCAAAACAGGTATTAATTTCAAAGAAATTTATCCACATAT	3998
Qy	3900	TGGTCAACACTGACCAACATGGTTTACAAACACTTCCAATGGACAGCCCTCGACCTTTAACTAT	3959
Db	3999	TGGTCAACACTGACCAACATGGTTTACAAACACTTCCAATGGACAGCCCTCGACCTTTAACTAT	4058
Qy	3960	TTTTCGACACGCACTGTGA	3978
Db	4059	TTTTCGACACGCACTGTGA	4077

Search completed: May 20, 2005, 09:10:55  
Job time : 16757 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 19:10:22 ; Search time 1981 Seconds  
(without alignments)  
11887.295 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcctgtgtaccagga.....ttttcagacagcactgtga 3978

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1980s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3978	100.0	3978	6	ABK92135
2	3978	100.0	3978	11	Adn39251 Prostate
3	3974.8	99.9	5271	12	Adh10611 Human can
4	3974.8	99.9	5284	12	Adh10612 Human can
5	3974.8	99.9	5833	12	Adh10624 Human can
6	3974.8	99.9	5862	12	Adh10626 Human can
7	3973.2	99.9	4231	2	Aaz30078 cDNA enco
8	3973.2	99.9	4231	5	Aah81778 Human dif
9	3973.2	99.9	4231	11	Adn39253 Cancer/an
10	3973.2	99.9	5832	13	Adr66822 Human pro
11	3973.2	99.9	5832	13	Adr65919 Human pro
12	3973.2	99.9	5870	10	Adb75177 Prostate
13	3971.6	99.8	4231	8	Abv75072 Human Dev
14	3966	99.7	6082	4	Aah93828 Human pro
15	3966	99.7	6082	4	Aas63921 Human pro
16	3966	99.7	6082	4	Aah85142 Human pro
17	3966	99.7	6082	5	Aca59729 Prostate
18	3966	99.7	6082	6	Adl95292 Human P51
19	3966	99.7	6082	8	Acc95456 Prostate
20	3966	99.7	6082	10	Adb13985 Human pro

21	3966	99.7	6082	10	ADG26401	Adg26401 Human pro
22	3965.4	99.7	4515	5	ABV24188	Abv24188 Human pro
23	3965.4	99.7	4515	5	ABV26511	Abv26511 Human pro
24	3965.4	99.7	4515	5	ABV20669	Abv20669 Human pro
25	3965.4	99.7	4515	5	ABV22410	Abv22410 Human pro
26	3965.4	99.7	4515	5	ABV24580	Abv24580 Human pro
27	3965.4	99.7	4515	5	ABV28224	Abv28224 Human pro
28	3899	98.0	3913	12	ADQ59423	Adq59423 Human can
29	3797.8	95.5	6140	4	AAH93829	Aah93829 Human pro
30	3797.8	95.5	6140	4	AAH63922	Aas63922 Human pro
31	3797.8	95.5	6140	4	AAH85143	Aah85143 Human pro
32	3797.8	95.5	6140	5	ACA59730	Acc59730 Prostate
33	3797.8	95.5	6140	6	ABL95293	AbL95293 Human P51
34	3797.8	95.5	6140	8	ACC95457	Acc95457 Prostate
35	3797.8	95.5	6140	10	ADB13986	Adb13986 Human pro
36	3797.8	95.5	6140	10	ADG26402	Adg26402 Human pro
37	3742.4	94.1	4395	8	ACC95747	Acc95747 Prostate
38	3742.4	94.1	4395	10	ADB14457	Adb14457 Expressio
39	3742.4	94.1	4395	10	ADG26980	Adg26980 Human pro
40	3741.8	94.1	3786	8	ACC95746	Acc95746 Prostate
41	3741.8	94.1	3786	10	ADB14456	Adb14456 Expressio
42	3741.8	94.1	3786	10	ADG26979	Adg26979 Human pro
43	2802.8	70.5	3521	12	ADH10613	Adh10613 Human can
44	2642.8	66.4	5550	12	ADQ59420	Adq59420 Human can
45	1294.2	32.5	3200	12	ADH10616	Adh10616 Human can

#### ALIGNMENTS

#### RESULT 1

ABK92135  
ID ABK92135 standard; DNA; 3978 BP.  
XX  
AC ABK92135;  
XX  
DT 15-AUG-2002 (first entry)  
XX  
DB Prostate cancer-associated DNA sequence #21.

XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;  
KW gene therapy; gene; ds.  
XX Mammalia.

XX WO2002030268-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-US032045.

XX 13-OCT-2000; 2000US-00687576.

XX 08-DEC-2000; 2000US-00733288.

XX 24-JAN-2001; 2001US-0263957P.

XX 16-MAR-2001; 2001US-0276791P.

XX 16-MAR-2001; 2001US-0276888P.

XX 06-APR-2001; 2001US-0281922P.

XX 24-APR-2001; 2001US-0286214P.

XX 30-APR-2001; 2001US-00847046.

XX 04-MAY-2001; 2001US-0288589P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevexi P;

XX WPI; 2002-471335/50.

XX P-PSDB; ABG61820.

XX Detecting a prostate cancer-associated transcript in a cell in a patient,

XX useful for diagnosing prostate cancer (pc) or screening modulators of PC,

XX by determining if prostate cancer-associated genes are expressed in a

XX prostate tissue.

XX Claim 22; Page 316; 436pp; English.

XX The present invention relates to methods of detecting a prostate cancer-  
 CC associated transcript in a cell from a patient. The method comprises  
 CC contacting a biological sample from the patient with prostate cancer-  
 CC associated polynucleotides (designated PC genes) that selectively  
 CC hybridise to a sequence that is at least 80% identical to them. The  
 CC prostate cancer-associated polynucleotide sequences are differentially  
 CC expressed in prostate tumour tissue or in prostate cancer and are derived  
 CC from the tissues of various organisms such as humans or other mammals  
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for  
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-  
 CC associated genes are useful for diagnosing or treating prostate cancer,  
 CC as well as for identifying modulators of prostate cancer or agents that  
 CC inhibit prostate cancer. The nucleic acid sequences are particularly  
 CC useful in gene therapy, as a vaccine or in antisense applications.  
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide  
 CC sequences

XX SQ Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 U; 0 Other;

Query Match 100.0%; Score 3978; DB 6; Length 3978;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCCGCTACAGAGGTTGAAGCCCAACCCGCTGCAGGACGGCAACCTCTGCTCA 60  
 Db 1 ATGCTGCCGCTACAGAGGTTGAAGCCCAACCCGCTGCAGGACGGCAACCTCTGCTCA 60

Qy 61 CGCGTGTTCTTCGGTGGCTCAATCCCTGTTTAAATTTGCCATTAACGGAGATTAGAG 120  
 Db 61 CGCGTGTTCTTCGGTGGCTCAATCCCTGTTTAAATTTGCCATTAACGGAGATTAGAG 120

Qy 121 GAAGATGATATGATTCAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180  
 Db 121 GAAGATGATATGATTCAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180

Qy 181 CAAGGTTCTGGGATAAAGAAAGTTTAAAGCTGAGAAATGAGCAACAGAGCCCTCTTTTA 240  
 Db 181 CAAGGTTCTGGGATAAAGAAAGTTTAAAGCTGAGAAATGAGCAACAGAGCCCTCTTTTA 240

Qy 241 ACAGAGCAATCATAAAGTTTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
 Db 241 ACAGAGCAATCATAAAGTTTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300

Qy 301 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCAATTTTTGGGAAATTTATTAATTTT 360  
 Db 301 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCAATTTTTGGGAAATTTATTAATTTT 360

Qy 361 GAAATTTATGATCCGATGGATTCGTGGCTTTGAAACACAGGTTACGCTATGCCACGGTG 420  
 Db 361 GAAATTTATGATCCGATGGATTCGTGGCTTTGAAACACAGGTTACGCTATGCCACGGTG 420

Qy 421 CTGACTTTTTCAGCGCTCATTTTCGGCTATCTGCATCACTTATATTTTATCAGTTTCAG 480  
 Db 421 CTGACTTTTTCAGCGCTCATTTTCGGCTATCTGCATCACTTATATTTTATCAGTTTCAG 480

Qy 481 TGTCTGGGATGAGTTACGATAGCCATATGTCATATGATTTATCGGAAGCACTTCGT 540  
 Db 481 TGTCTGGGATGAGTTACGATAGCCATATGTCATATGATTTATCGGAAGCACTTCGT 540

Qy 541 CTTAGTAAATGATGGGCAAGAGCAACCAACAGGCGCAGATAGTCAATCTGCTGTCCAAT 600  
 Db 541 CTTAGTAAATGATGGGCAAGAGCAACCAACAGGCGCAGATAGTCAATCTGCTGTCCAAT 600

Qy 601 GATGTGAACAGTTTGTATCAGGTGCAAGTGTCTTACACTTCCGTGGGAGGACCACTG 660  
 Db 601 GATGTGAACAGTTTGTATCAGGTGCAAGTGTCTTACACTTCCGTGGGAGGACCACTG 660

Qy 661 CAGGCGATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCTTGTGGG 720  
 Db 661 CAGGCGATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCTTGTGGG 720

Qy 721 ATGGCAGTCTTAATCATTCTCCTGCCCTTGCAAAAGCTGTTTGGGAGTGTCTTCATCA 780  
 Db 721 ATGGCAGTCTTAATCATTCTCCTGCCCTTGCAAAAGCTGTTTGGGAGTGTCTTCATCA 780

Qy 781 CTGAGGAGTAAACTGCAACTTTTCACGATGTCAGGATCAGGACCATGAATGAAGTTATA 840  
 Db 781 CTGAGGAGTAAACTGCAACTTTTCACGATGTCAGGATCAGGACCATGAATGAAGTTATA 840

Qy 841 ACTGGTATAAGGATAATAAAATGTACGCTGGGAAAAGTCATTTTCAAATCTTATTAACC 900  
 Db 841 ACTGGTATAAGGATAATAAAATGTACGCTGGGAAAAGTCATTTTCAAATCTTATTAACC 900

Qy 901 AATTGGAAGAAGGAGATTTCAGAGTTCTGAGAGTTCTCCCTCAGGGGATGAAT 960  
 Db 901 AATTGGAAGAAGGAGATTTCAGAGTTCTGAGAGTTCTCCCTCAGGGGATGAAT 960

Qy 961 TTGGCTTCGTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCAACCACCTAGCTG 1020  
 Db 961 TTGGCTTCGTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTGACCTTCAACCACCTAGCTG 1020

Qy 1021 CTCTCGGCAGTGTGATCACAGCCAGCCGCTGTTCTGTGGCAAGTGCCTGTATGGGGCT 1080  
 Db 1021 CTCTCGGCAGTGTGATCACAGCCAGCCGCTGTTCTGTGGCAAGTGCCTGTATGGGGCT 1080

Qy 1081 GTGGGCTGACGGTTACCTCTTCTCCCTCAGCCATTGAGAGGTTGTCAGAGGCAATC 1140  
 Db 1081 GTGGGCTGACGGTTACCTCTTCTCCCTCAGCCATTGAGAGGTTGTCAGAGGCAATC 1140

Qy 1141 GTCAGCATCCGAAGAATCCAGACCTTTTCTACTTCTGATGAGATATCACAGCGCAACCGT 1200  
 Db 1141 GTCAGCATCCGAAGAATCCAGACCTTTTCTACTTCTGATGAGATATCACAGCGCAACCGT 1200

Qy 1201 CAGCTGCCGTGAGATGTTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT 1260  
 Db 1201 CAGCTGCCGTGAGATGTTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT 1260

Qy 1261 AAGCATCAGAGCCCCCACTCTACAGGCTTCTTCTTACTGTCAGACCTGGCGGAATTG 1320  
 Db 1261 AAGCATCAGAGCCCCCACTCTACAGGCTTCTTCTTACTGTCAGACCTGGCGGAATTG 1320

Qy 1321 TTAGCTGTGCTGGCCCGCTGGGAGAGGAAAGTCATCACTGTTAACTGCGCTCGCTCGGG 1380  
 Db 1321 TTAGCTGTGCTGGCCCGCTGGGAGAGGAAAGTCATCACTGTTAACTGCGCTCGCTCGGG 1380

Qy 1381 GAATGTCGCCCAAGTCACGGGCTGGTCAGGTCGATGGAAGATTTGCTATGTCTCAG 1440  
 Db 1381 GAATGTCGCCCAAGTCACGGGCTGGTCAGGTCGATGGAAGATTTGCTATGTCTCAG 1440

Qy 1441 CAGCCCTGGGCTGTTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
 Db 1441 CAGCCCTGGGCTGTTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500

Qy 1501 AAGGAACGATATGAAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTTACAGCTGTG 1560  
 Db 1501 AAGGAACGATATGAAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTTACAGCTGTG 1560

Qy 1561 GAGATGGTGTGATCTGCTGATAGGAGATCGGGGAAACCAAGCTGAGTGGAGGCGAGAA 1620  
 Db 1561 GAGATGGTGTGATCTGCTGATAGGAGATCGGGGAAACCAAGCTGAGTGGAGGCGAGAA 1620

Qy 1621 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1680  
 Db 1621 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1680

Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
 Db 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740

Qy 1741 ATTTTGCATGAGAAGATCAAAATTTTATGATGATCATCATGTTGACGTACCTCAAAAGCTGCA 1800  
 Db 1741 ATTTTGCATGAGAAGATCAAAATTTTATGATGATCATCATGTTGACGTACCTCAAAAGCTGCA 1800

QY 1801 AGTCAGATCTTGATATTAATGAAAGATGGTAAATGGTGAGAGGGGACTTACACTGAGTTC 1860  
DB 1801 AGTCAGATCTTGATATTAATGAAAGATGGTAAATGGTGAGAGGGGACTTACACTGAGTTC 1860  
QY 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGAGAAAGTGAACAA 1920  
DB 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGAGAAAGTGAACAA 1920  
QY 1921 CCTCCAGTTCAGGAATCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCCGTTTGG 1980  
DB 1921 CCTCCAGTTCAGGAATCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCCGTTTGG 1980  
QY 1981 TCTCAACAACTTCTAGACCTCTTGAAGATGGTCTCTGAGAGCCCAAGATACAGAG 2040  
DB 1981 TCTCAACAACTTCTAGACCTCTTGAAGATGGTCTCTGAGAGCCCAAGATACAGAG 2040  
QY 2041 AATGTCCTCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2100  
DB 2041 AATGTCCTCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2100  
QY 2101 TATAAGAAATTAATTCAGAGCTGGTCTCAGTGAATGTCTTCAATTTTCTTATTTCTCCTA 2160  
DB 2101 TATAAGAAATTAATTCAGAGCTGGTCTCAGTGAATGTCTTCAATTTTCTTATTTCTCCTA 2160  
QY 2161 AACACTGCAGCTCAGGTTGCCATATGTCTTCAAGATTTGGTGGCTTTCATACTGGGCAAC 2220  
DB 2161 AACACTGCAGCTCAGGTTGCCATATGTCTTCAAGATTTGGTGGCTTTCATACTGGGCAAC 2220  
QY 2221 AACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAATGTAAACGAGAGCTAGAT 2280  
DB 2221 AACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAATGTAAACGAGAGCTAGAT 2280  
QY 2281 CTTAACTGGTACTTGAAGATTTATTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATA 2340  
DB 2281 CTTAACTGGTACTTGAAGATTTATTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATA 2340  
QY 2341 GCAAGATCTCTATTTGGTATTTCTAGTCTCTTGTAACTCTTCAAACTTTTGCACAAACAA 2400  
DB 2341 GCAAGATCTCTATTTGGTATTTCTAGTCTCTTGTAACTCTTCAAACTTTTGCACAAACAA 2400  
QY 2401 ATGTTTGAGTCAATTTGAAAGCTCCGGTATTTATCTTTGATAGAAATCCAAATAGGAAGA 2460  
DB 2401 ATGTTTGAGTCAATTTGAAAGCTCCGGTATTTATCTTTGATAGAAATCCAAATAGGAAGA 2460  
QY 2461 ATTTTAAATCGTTTCTCAAAGACATTTGACACTTTGATGATGATTTGCTGCGCTGACGTTT 2520  
DB 2461 ATTTTAAATCGTTTCTCAAAGACATTTGACACTTTGATGATGATTTGCTGCGCTGACGTTT 2520  
QY 2521 TTAGATTTTCACAGACATTTGCTACAAAGTGGTGGTGGTCTCTGTTGGCTGTGGCCGCTG 2580  
DB 2521 TTAGATTTTCACAGACATTTGCTACAAAGTGGTGGTGGTCTCTGTTGGCTGTGGCCGCTG 2580  
QY 2581 ATTCTTTGGATTCGGAATFACCTTTGGTTCCCTTTGGGAATCAATTTTCAATTTTCTTCCGCGA 2640  
DB 2581 ATTCTTTGGATTCGGAATFACCTTTGGTTCCCTTTGGGAATCAATTTTCAATTTTCTTCCGCGA 2640  
QY 2641 TATTTTGGAAAGCTCAAGAGATGTGAAGCGCTGGAATCTCAACTTCGAGGTCACAGT 2700  
DB 2641 TATTTTGGAAAGCTCAAGAGATGTGAAGCGCTGGAATCTCAACTTCGAGGTCACAGT 2700  
QY 2701 TTTTCCCACTTGTCACTCTCTCCAGGGCTCTGGACCAATCCGGGCAATCAAAAGCAGAA 2760  
DB 2701 TTTTCCCACTTGTCACTCTCTCCAGGGCTCTGGACCAATCCGGGCAATCAAAAGCAGAA 2760  
QY 2761 GAGAGGTGTGAGGAATCTGTTTGAATGACACAGGATTTAATTACAGAGGCTTGGTTCTTG 2820  
DB 2761 GAGAGGTGTGAGGAATCTGTTTGAATGACACAGGATTTAATTACAGAGGCTTGGTTCTTG 2820  
QY 2821 TTTTGTGACAGCTCCCGCTGGTTCGGCTCGGTCTGATGCCATCTGTGCCATGTTTGTG 2880  
DB 2821 TTTTGTGACAGCTCCCGCTGGTTCGGCTCGGTCTGATGCCATCTGTGCCATGTTTGTG 2880  
QY 2881 ATCATCGTTGGCTTGGGTCCCTGATTTCTGCGCAAAACTCTGAGTCCGGGAGGTTGGT 2940

DB 2881 ATCATCGTTGGCTTGGGTCCCTGATTTCTGCAAAACTCTCTGGATCCGGGACAGTTCGT 2940  
QY 2941 TTGGCACTGTCTCTATGCTTCCCTCAGCTCATGGGATGTTTCACTGGTGTGTTTCGACAAAGT 3000  
DB 2941 TTGGCACTGTCTCTATGCTTCCCTCAGCTCATGGGATGTTTCACTGGTGTGTTTCGACAAAGT 3000  
QY 3001 GCTGAAGTCTGAGAAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACTTGAA 3060  
DB 3001 GCTGAAGTCTGAGAAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACTTGAA 3060  
QY 3061 AAAGAAAGCACTTTGGGAATATCAGAAACGCCACCAACAGCTGGCCCCATGAAGAGTGT 3120  
DB 3061 AAAGAAAGCACTTTGGGAATATCAGAAACGCCACCAACAGCTGGCCCCATGAAGAGTGT 3120  
QY 3121 ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTCTGGTACTGAAGCAT 3180  
DB 3121 ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTCTGGTACTGAAGCAT 3180  
QY 3181 CTGACAGCACTCATTTAAATCAAGAAAGGTTGGCAATTTGGGAAAGAACCGGAGCTTGA 3240  
DB 3181 CTGACAGCACTCATTTAAATCAAGAAAGGTTGGCAATTTGGGAAAGAACCGGAGCTTGA 3240  
QY 3241 AAAAGTTCCCTCATCTCAGGCCCTTTTATGATTTGTGAGAACCCGAGGTAAATTTGGATT 3300  
DB 3241 AAAAGTTCCCTCATCTCAGGCCCTTTTATGATTTGTGAGAACCCGAGGTAAATTTGGATT 3300  
QY 3301 GATAAGATCTTGACAACTGAAATTTGGACTTCAAGATTTAGGAAGAAATGTCAATCAT 3360  
DB 3301 GATAAGATCTTGACAACTGAAATTTGGACTTCAAGATTTAGGAAGAAATGTCAATCAT 3360  
QY 3361 CCTCAGGAACCTGTTTGTTCCTGGAACCAATGAGGAAACCTTGGATCCCTTTTAAATGAG 3420  
DB 3361 CCTCAGGAACCTGTTTGTTCCTGGAACCAATGAGGAAACCTTGGATCCCTTTTAAATGAG 3420  
QY 3421 CACAAGATCTGGAACCTGTTGCTTCAAGAGGTACAACTTAAAGAAACCAATTTGAA 3480  
DB 3421 CACAAGATCTGGAACCTGTTGCTTCAAGAGGTACAACTTAAAGAAACCAATTTGAA 3480  
QY 3481 GATCTTCTGTTAAATGGAATGGAATGAGATTTAGCAGAACTCAGATCCCAATTTTAGTGTGGA 3540  
DB 3481 GATCTTCTGTTAAATGGAATGGAATGAGATTTAGCAGAACTCAGATCCCAATTTTAGTGTGGA 3540  
QY 3541 CAAAGCAACTGTGTGCTTGGCCCTTGGCAGGGCAATCTCAGGAAATCAGATATTTATTT 3600  
DB 3541 CAAAGCAACTGTGTGCTTGGCCCTTGGCAGGGCAATCTCAGGAAATCAGATATTTATTT 3600  
QY 3601 GATGAAGCGACGGCAAAATGTGGATCCAAAGAACTGATGAGTTAAATCAAAAGAAATCCGG 3660  
DB 3601 GATGAAGCGACGGCAAAATGTGGATCCAAAGAACTGATGAGTTAAATCAAAAGAAATCCGG 3660  
QY 3661 GAGAAATTTGCCCACTGACCGTCTTAACTTTGACACAGATTTGAACACCATTTATTGAC 3720  
DB 3661 GAGAAATTTGCCCACTGACCGTCTTAACTTTGACACAGATTTGAACACCATTTATTGAC 3720  
QY 3721 AGGCAAGAAATATGTTTGTAGATTTAGGAACTGAAAGAAATATGATGAGCCGTATGTT 3780  
DB 3721 AGGCAAGAAATATGTTTGTAGATTTAGGAACTGAAAGAAATATGATGAGCCGTATGTT 3780  
QY 3781 TTGCTGCAAAATTAAGAGAGCTTATTTTCAAGATGTTGCAACAACTGGGCAAGGCGAGAA 3840  
DB 3781 TTGCTGCAAAATTAAGAGAGCTTATTTTCAAGATGTTGCAACAACTGGGCAAGGCGAGAA 3840  
QY 3841 GCGCTGCCCTCATCTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATTCACATATT 3900  
DB 3841 GCGCTGCCCTCATCTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATTCACATATT 3900  
QY 3901 GGTTCACACTGACCACTGTTTCAAAACACTTCCAAATGAGCAGCCCTCGACCTTAACATT 3960  
DB 3901 GGTTCACACTGACCACTGTTTCAAAACACTTCCAAATGAGCAGCCCTCGACCTTAACATT 3960  
QY 3961 TTGAGACAGCACTGTGA 3978

Db 3961 TTCGAGACAGCACTGTGA 3978  
 RESULT 2  
 ADN39251  
 ADN39251 standard; cDNA; 3978 BP.  
 XX  
 AC ADN39251;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:569.  
 XX  
 KW Human; differential expression; cancer; angiogenic disorder;  
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
 KW inflammatory disease; autoimmune disease;  
 KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
 KW vulnerary; gene therapy; vaccine; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003042661-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 13-NOV-2002; 2002WO-US036810.  
 XX  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 21-NOV-2001; 2001US-0332464P.  
 PR 29-NOV-2001; 2001US-0334393P.  
 PR 03-DEC-2001; 2001US-0335394P.  
 PR 14-DEC-2001; 2001US-0340376P.  
 PR 08-JAN-2002; 2002US-0347211P.  
 PR 10-JAN-2002; 2002US-0347349P.  
 PR 08-FEB-2002; 2002US-0355250P.  
 PR 13-FEB-2002; 2002US-0356714P.  
 PR 20-FEB-2002; 2002US-0359077P.  
 PR 29-MAR-2002; 2002US-0368809P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-0372426P.  
 PR 05-JUN-2002; 2002US-0386614P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397775P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
 XX  
 DR WPI; 2003-468649/44.  
 DR P-PSDB; ADN39252.  
 XX  
 PT Determining the presence or absence of a pathological cell in a patient,  
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
 PT a nucleic acid in a biological sample.  
 XX  
 PS Claim 8; SEQ ID NO 569; 1385pp; English.  
 XX  
 CC The invention relates to nucleic acids and proteins (ADN38693-ADN40064)  
 CC whose expression is upregulated or downregulated in specific cancers or  
 CC other diseases such as angiogenic or fibrotic disorders, and to methods  
 CC of determining the presence or absence of a pathological cell in a  
 CC patient by detecting a nucleic acid at least 80% identical to those of  
 CC the invention or by detecting a polypeptide of the invention. The  
 CC invention also relates to expression vectors and host cells comprising a  
 CC nucleic acid of the invention; antibodies which specifically bind a  
 CC polypeptide of the invention; use of such antibodies for drug targeting;  
 CC and methods of screening for modulators of activity or expression of the  
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,

CC antibodies and methods are useful for diagnosing, prognosing and treating  
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 CC neovascularisation syndromes, scarring and uterine fibroids. They may  
 CC also be useful in wound healing and in contraception. The present  
 CC sequence represents a nucleic acid sequence of the invention.  
 XX  
 SQ Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 3978; DB 11; Length 3978;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGCTGCCCTGTACACAGGAGGTGAGCCCAACCCGCTGCAGGACCGGAACCTCTGCTCA 60  
 Db 1 ATGCTGCCCTGTACACAGGAGGTGAGCCCAACCCGCTGCAGGACCGGAACCTCTGCTCA 60  
 Qy 61 CGCGTGTCTTCTGCTGGCTCAATCCCTCTGTTAAATTTGGCCATAAACGGAGATTAGAG 120  
 Db 61 CGCGTGTCTTCTGCTGGCTCAATCCCTCTGTTAAATTTGGCCATAAACGGAGATTAGAG 120  
 Qy 121 GAAGATGATATGATATTCAGTGTCTGCCAAGAGACCGCTCACAGCACCTTTGGAGAGATTG 180  
 Db 121 GAAGATGATATGATATTCAGTGTCTGCCAAGAGACCGCTCACAGCACCTTTGGAGAGATTG 180  
 Qy 181 CAAGGTTCTGGGATTAAGAGTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTA 240  
 Db 181 CAAGGTTCTGGGATTAAGAGTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTA 240  
 Qy 241 ACAAGACAATCAATAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTA 300  
 Db 241 ACAAGACAATCAATAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTA 300  
 Qy 301 ATTGAGGAAAGTGCAAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATAATTTT 360  
 Db 301 ATTGAGGAAAGTGCAAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATAATTTT 360  
 Qy 361 GAAAAATATGATCCCATGGATCTGTGGCTTTGAAACACAGGTACGCTATGCCACGGT 420  
 Db 361 GAAAAATATGATCCCATGGATCTGTGGCTTTGAAACACAGGTACGCTATGCCACGGT 420  
 Qy 421 CTGACTTTTTCACGCTCATTTTGGCTATATCTGATCACTATATTTTATCAGTTTCA 480  
 Db 421 CTGACTTTTTCACGCTCATTTTGGCTATATCTGATCACTATATTTTATCAGTTTCA 480  
 Qy 481 TGTCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACTTCGT 540  
 Db 481 TGTCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACTTCGT 540  
 Qy 541 CTTAGTAACATGGCCATGGGGAGACAAACACAGCCAGATAGTCAATCTGCTCCAAT 600  
 Db 541 CTTAGTAACATGGCCATGGGGAGACAAACACAGCCAGATAGTCAATCTGCTCCAAT 600  
 Qy 601 GATGTAAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGACGAGCACTG 660  
 Db 601 GATGTAAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGACGAGCACTG 660  
 Qy 661 CAGCGGATGCGAGTACCTGCTTACTCTGATGAGATAGGAATATGCTGCTTCTGCTGG 720  
 Db 661 CAGCGGATGCGAGTACCTGCTTACTCTGATGAGATAGGAATATGCTGCTTCTGCTGG 720  
 Qy 721 ATGGCAGTCTTAATCATTTCTGCTCCCTTGCARAGCTGTTTGGGAAGTTCTCTCATCA 780  
 Db 721 ATGGCAGTCTTAATCATTTCTGCTCCCTTGCARAGCTGTTTGGGAAGTTCTCTCATCA 780  
 Qy 781 CTGAGGAGTAAACTGCAACTTTTCAAGATGCGGATCAGGATCAGGACCATGAATGAATTA 840  
 Db 781 CTGAGGAGTAAACTGCAACTTTTCAAGATGCGGATCAGGATCAGGACCATGAATGAATTA 840  
 Qy 841 ACTGGTATAGGATTAATAAATAATGACCTGGGAAAAAGTCATTTTCAATCTTATTACC 900  
 Db 841 ACTGGTATAGGATTAATAAATAATGACCTGGGAAAAAGTCATTTTCAATCTTATTACC 900

Qy	901	AATTGTGAAAGAAAGGAGATTTC	CAAGATTCTG	AAGAGTTCTCCTCCCTCAGGGGATGAAT	960	
Db	901	AAATTGAGAAAGAGGAGATTTC	CAAGATTCTG	AAGAGTTCTCCTCCCTCAGGGGATGAAT	960	
Qy	961	TTGGCTTCGTTTTT	CAGTGCAGCAAAATCATCGT	TTTGGAGCTTTCACCACTACGTG	1020	
Db	961	TTGGCTTCGTTTTT	CAGTGCAGCAAAATCATCGT	TTTGGAGCTTTCACCACTACGTG	1020	
Qy	1021	CTCCTCGGCAAGTGTGATC	CACAGCCGCGGTGTT	CGTGGCAGTGCAGCTGTATGGGGCT	1080	
Db	1021	CTCCTCGGCAAGTGTGATC	CACAGCCGCGGTGTT	CGTGGCAGTGCAGCTGTATGGGGCT	1080	
Qy	1081	GTGGGTGACGGTTAC	CCCTCTTCTTCCCTCAGCCAT	TTGAGAGGGTGTACAGAGCAATC	1140	
Db	1081	GTGGGTGACGGTTAC	CCCTCTTCTTCCCTCAGCCAT	TTGAGAGGGTGTACAGAGCAATC	1140	
Qy	1141	GTGAGCATCCGAGAAATCC	GAGACCTTTTGTCTACT	TGATGAGATATCACAGCGCAACGGT	1200	
Db	1141	GTGAGCATCCGAGAAATCC	GAGACCTTTTGTCTACT	TGATGAGATATCACAGCGCAACGGT	1200	
Qy	1201	CAGCTGCCGTGATG	GTGAAAGATGGTGCATG	TCAGGAGTTTACTTGTCTTTTGGAT	1260	
Db	1201	CAGCTGCCGTGATG	GTGAAAGATGGTGCATG	TCAGGAGTTTACTTGTCTTTTGGAT	1260	
Qy	1261	AAGGCATCAGAGACCC	CAACTCTA	CAAGGCCCTTTCTTTACTGT	CAGACCTGGCGAATTG	1320
Db	1261	AAGGCATCAGAGACCC	CAACTCTA	CAAGGCCCTTTCTTTACTGT	CAGACCTGGCGAATTG	1320
Qy	1321	TTAGCTGTGTCGGCCG	GTGGAGCAGGAGTCAT	CACTGTTAAGTGGCGTCTCGG	1380	
Db	1321	TTAGCTGTGTCGGCCG	GTGGAGCAGGAGTCAT	CACTGTTAAGTGGCGTCTCGG	1380	
Qy	1381	GAATTGGCCCAAGT	CAAGGCTGCTCAGCTGCAT	GTGAGAAATGGCTATGCTCTCAG	1440	
Db	1381	GAATTGGCCCAAGT	CAAGGCTGCTCAGCTGCAT	GTGAGAAATGGCTATGCTCTCAG	1440	
Qy	1441	CAGCCCTGGGTGTTCT	CGGGAACCTC	GAGGAGTAATATTTTATTTGGGAAGAAATACGAA	1500	
Db	1441	CAGCCCTGGGTGTTCT	CGGGAACCTC	GAGGAGTAATATTTTATTTGGGAAGAAATACGAA	1500	
Qy	1501	AAGAACGATATGAAAAG	TCATAAAGCTTGTGCTCT	GAAAAAGGATTTACAGCTGTTG	1560	
Db	1501	AAGAACGATATGAAAAG	TCATAAAGCTTGTGCTCT	GAAAAAGGATTTACAGCTGTTG	1560	
Qy	1561	GAGATGCTGATCTG	ATGATAGGAGATCGGGGAA	CCACGCTGAGTGGAGGSCAGAAA	1620	
Db	1561	GAGATGCTGATCTG	ATGATAGGAGATCGGGGAA	CCACGCTGAGTGGAGGSCAGAAA	1620	
Qy	1621	GCACGGTAAACCTT	GCAAGAGCAGTGTAT	CAAGATGCTGACATCTATCTCTGGACGAT	1680	
Db	1621	GCACGGTAAACCTT	GCAAGAGCAGTGTAT	CAAGATGCTGACATCTATCTCTGGACGAT	1680	
Qy	1681	CCTCTCAGTGAGATG	CGGAAAGTTAGCAGACA	CTTGTGTAATTTGTCAA	1740	
Db	1681	CCTCTCAGTGAGATG	CGGAAAGTTAGCAGACA	CTTGTGTAATTTGTCAA	1740	
Qy	1741	ATTTTGATGAGAGATC	ACAATTTTATGATCTCAT	CAGTTGCACTACCTCAAGCTGCA	1800	
Db	1741	ATTTTGATGAGAGATC	ACAATTTTATGATCTCAT	CAGTTGCACTACCTCAAGCTGCA	1800	
Qy	1801	AGTCAGATTCTGATAT	TGAAAGATGGTAAAT	TGTCAGAGGGGACTTACACTGAGTTC	1860	
Db	1801	AGTCAGATTCTGATAT	TGAAAGATGGTAAAT	TGTCAGAGGGGACTTACACTGAGTTC	1860	
Qy	1861	CTAAATCTGGTATAG	ATTTTGGCTCCCTTTT	TAAAGAGGATATGAGGAAAGTGAACAA	1920	
Db	1861	CTAAATCTGGTATAG	ATTTTGGCTCCCTTTT	TAAAGAGGATATGAGGAAAGTGAACAA	1920	
Qy	1921	CCTCCAGTCCAGAA	CTCCACACTAAGGAAT	CGTACCTTCTCAGAGTCTTCGGTTTG	1980	
Db	1921	CCTCCAGTCCAGAA	CTCCACACTAAGGAAT	CGTACCTTCTCAGAGTCTTCGGTTTG	1980	
Qy	1981	TCTCAACAATCTT	CTAGACCTCCTT	TGAAAGATGGTGTCTCTGGAGAGC	CAAGATACAGAG	2040

Db	1981	TCTCAACAATCTT	CTAGACCTCCTT	TGAAAGATGGTGTCTCTGGAGAGC	CAAGATACAGAG	2040	
Qy	2041	AATGTCACAGTTAC	CATCATCAGAGGAA	CCGTTCTGAAGGAAAGTTGGTTTTCAGGCC	2100		
Db	2041	AATGTCACAGTTAC	CATCATCAGAGGAA	CCGTTCTGAAGGAAAGTTGGTTTTCAGGCC	2100		
Qy	2101	TATAAGAAATAC	TTTTCAGAGCTGGTGTCT	CACCTGGAATGTCTTCA	TTTTCCTTATTCCTTA	2160	
Db	2101	TATAAGAAATAC	TTTTCAGAGCTGGTGTCT	CACCTGGAATGTCTTCA	TTTTCCTTATTCCTTA	2160	
Qy	2161	AACACTGCAGT	CAGGTTGCTATG	TGCTTCAAGATTGGTGGCTTTTCA	TACTGGGCAAAAC	2220	
Db	2161	AACACTGCAGT	CAGGTTGCTATG	TGCTTCAAGATTGGTGGCTTTTCA	TACTGGGCAAAAC	2220	
Qy	2221	AAACAAAGTATG	CTAAATGTCACTG	TAAATGGAGGAGAAATG	TAAACCGAGAAGCTAGAT	2280	
Db	2221	AAACAAAGTATG	CTAAATGTCACTG	TAAATGGAGGAGAAATG	TAAACCGAGAAGCTAGAT	2280	
Qy	2281	CTTAACTGGTAC	TTAGGAAATTTAT	TTCAGGTTTAACTGTAGCTAC	CGTTCCTTTTGGCATA	2340	
Db	2281	CTTAACTGGTAC	TTAGGAAATTTAT	TTCAGGTTTAACTGTAGCTAC	CGTTCCTTTTGGCATA	2340	
Qy	2341	GCAAGATCTCTA	TTGGTATTTCTAG	CTCCTTGTAACTCTTCA	CAAACTTTTGCACAAACAA	2400	
Db	2341	GCAAGATCTCTA	TTGGTATTTCTAG	CTCCTTGTAACTCTTCA	CAAACTTTTGCACAAACAA	2400	
Qy	2401	ATGTTTTCAGTCA	ATTTCTGAAGCTCC	CGGTATTATTTCTGATAGAAAT	CCAATAGGAAGA	2460	
Db	2401	ATGTTTTCAGTCA	ATTTCTGAAGCTCC	CGGTATTATTTCTGATAGAAAT	CCAATAGGAAGA	2460	
Qy	2461	ATTTTAAATCGT	TTCTCCAAAGACAT	TGGACACTTGGATGATTTG	CTGCCCTGACGCTTT	2520	
Db	2461	ATTTTAAATCGT	TTCTCCAAAGACAT	TGGACACTTGGATGATTTG	CTGCCCTGACGCTTT	2520	
Qy	2521	TTAGATTTCA	TCACAGACATTTG	CTCAAGTGGTGGTGTCTCTGTGGCTGTG	CGCCGTG	2580	
Db	2521	TTAGATTTCA	TCACAGACATTTG	CTCAAGTGGTGGTGTCTCTGTGGCTGTG	CGCCGTG	2580	
Qy	2581	ATTCCTTGGAT	CCCAATACCTTGGT	TCCCTTGGAAATCATTTT	CAATTTTCTTCGGCGA	2640	
Db	2581	ATTCCTTGGAT	CCCAATACCTTGGT	TCCCTTGGAAATCATTTT	CAATTTTCTTCGGCGA	2640	
Qy	2641	TATTTTGGAAAC	CGTCAAGAGATGT	CAAGCGCTCGAATCTACA	ACTCGGAGTCCAGTG	2700	
Db	2641	TATTTTGGAAAC	CGTCAAGAGATGT	CAAGCGCTCGAATCTACA	ACTCGGAGTCCAGTG	2700	
Qy	2701	TTTTTCCCACT	TTGTCATCTTCT	CCAGGGCTCTGGA	CCATCCGGGCATACAAAGCAAA	2760	
Db	2701	TTTTTCCCACT	TTGTCATCTTCT	CCAGGGCTCTGGA	CCATCCGGGCATACAAAGCAAA	2760	
Qy	2761	GAGAGGTGT	CAGGAACTGTTT	TGATGACACAGGATTTT	TACATTCAGAGGCTTGGTCTTG	2820	
Db	2761	GAGAGGTGT	CAGGAACTGTTT	TGATGACACAGGATTTT	TACATTCAGAGGCTTGGTCTTG	2820	
Qy	2821	TTTTTGAACA	AGCTCCCGCTGTT	CGCGTCTGATG	CCATCTGTGCCATGTGTC	2880	
Db	2821	TTTTTGAACA	AGCTCCCGCTGTT	CGCGTCTGATG	CCATCTGTGCCATGTGTC	2880	
Qy	2881	ATCATCGT	TTCCTTGGGTCC	CTGATTTCTGGCA	AAAACTCTCTGGATCCGGG	CAGGTTGGT	2940
Db	2881	ATCATCGT	TTCCTTGGGTCC	CTGATTTCTGGCA	AAAACTCTCTGGATCCGGG	CAGGTTGGT	2940
Qy	2941	TTGGCACT	GTCTTATG	CCCTCAGCTCAT	TGGGATGTTTTCAGTGTGTT	TCGACAAAGT	3000
Db	2941	TTGGCACT	GTCTTATG	CCCTCAGCTCAT	TGGGATGTTTTCAGTGTGTT	TCGACAAAGT	3000
Qy	3001	GCTGAAGT	TCAGAAATATG	ATCTCAGTAGA	AAAGGTCATTGAAATAC	CACAGACCTTCAA	3060
Db	3001	GCTGAAGT	TCAGAAATATG	ATCTCAGTAGA	AAAGGTCATTGAAATAC	CACAGACCTTCAA	3060
Qy	3061	AAAGAAGC	ACTTTGGGAATAT	CAAAAACGCC	CAACAGCTCGCC	CCCATGAAGGATG	3120
Db	3061	AAAGAAGC	ACTTTGGGAATAT	CAAAAACGCC	CAACAGCTCGCC	CCCATGAAGGATG	3120



Db 3061 AAGAAGCACCTTGGGAATATCAGAAAGCCACCACAGCCTCGGCCCATGAAGGAGTG 3120  
 Qy 3121 ATAATCTTTGACAAATGAACTTCATGTACAGTCAGGTGGGCTCTGGTACTGAAGCAT 3180  
 Db 3121 ATAATCTTTGACAAATGAACTTCATGTACAGTCAGGTGGGCTCTGGTACTGAAGCAT 3180  
 Qy 3181 CTGACAGCACTCATTAATCACAAGAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
 Db 3181 CTGACAGCACTCATTAATCACAAGAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
 Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATGTGAGAACCCGAGTAAATTTGGATT 3300  
 Db 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATGTGAGAACCCGAGTAAATTTGGATT 3300  
 Qy 3301 GATAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCAT 3360  
 Db 3301 GATAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCAT 3360  
 Qy 3361 CCTCAGCAACTGTTTGTTCACCTGGAAACATAGAGAAACCTGGATCCCTTTAATGAG 3420  
 Db 3361 CCTCAGCAACTGTTTGTTCACCTGGAAACATAGAGAAACCTGGATCCCTTTAATGAG 3420  
 Qy 3421 CACACGGATGAGGAACCTGTGAATGCTTCAACAGAGGTACAACTTAAAGAAACCAATTGAA 3480  
 Db 3421 CACACGGATGAGGAACCTGTGAATGCTTCAACAGAGGTACAACTTAAAGAAACCAATTGAA 3480  
 Qy 3481 GATCTTCTGTTAAATGGATGACTGAATTAGCAGAAATCAGATCCAAATTTAGTGTGGA 3540  
 Db 3481 GATCTTCTGTTAAATGGATGACTGAATTAGCAGAAATCAGATCCAAATTTAGTGTGGA 3540  
 Qy 3541 CAAAGCAACTGTGTGCTTGCCTGGCAGGCAATCTCAGGAAATCAGATATGATTAAT 3600  
 Db 3541 CAAAGCAACTGTGTGCTTGCCTGGCAGGCAATCTCAGGAAATCAGATATGATTAAT 3600  
 Qy 3601 GATGAAGCGAGCGCAATGTGGATCCAGAACTGATGAGTTAATACAAAATAAATCCGG 3660  
 Db 3601 GATGAAGCGAGCGCAATGTGGATCCAGAACTGATGAGTTAATACAAAATAAATCCGG 3660  
 Qy 3661 GAGAAATTTGCCACTGACCGTCTAACCAATTCACACAGATTTGAACCAATTAATTGAC 3720  
 Db 3661 GAGAAATTTGCCACTGACCGTCTAACCAATTCACACAGATTTGAACCAATTAATTGAC 3720  
 Qy 3721 AGGCACAGATAATGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3780  
 Db 3721 AGGCACAGATAATGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3780  
 Qy 3781 TTGCTGCAAAATAAAGAGAGCTATTTTACAGATGGTGCAACAACTGGGCAAGGCAGAA 3840  
 Db 3781 TTGCTGCAAAATAAAGAGAGCTATTTTACAGATGGTGCAACAACTGGGCAAGGCAGAA 3840  
 Qy 3841 GCCGCTGCCCTCAGTGAACAGCAACAGGTATACCTTCAAGAAATTTATCCACATATT 3900  
 Db 3841 GCCGCTGCCCTCAGTGAACAGCAACAGGTATACCTTCAAGAAATTTATCCACATATT 3900  
 Qy 3901 GGTCACTGACCACTGTTTACAAACACTTCCCAATGGACAGCCCTCGACCTTAACTATT 3960  
 Db 3901 GGTCACTGACCACTGTTTACAAACACTTCCCAATGGACAGCCCTCGACCTTAACTATT 3960  
 Qy 3961 TTCGAGACAGCACTGTGA 3978  
 Db 3961 TTCGAGACAGCACTGTGA 3978

RESULT 3  
 ADH10611  
 ID ADH10611 standard; DNA; 5271 BP.  
 XX  
 AC ADH10611;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Human cancer-related polynucleotide, SEQ ID 1.  
 .XX

Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.  
 Homo sapiens.  
 W02003104404-A2.  
 18-DEC-2003.  
 05-JUN-2003; 2003WO-US017772.  
 06-JUN-2002; 2002US-0386651P.  
 (AVAL-) AVALON PHARM INC.  
 Ebner R;  
 WPI; 2004-062332/06.  
 Identifying agents that modulate the activity of cancer-related gene, useful for treating or diagnosing prostate cancer comprising contacting a compound with a cell containing a gene under conditions promoting expression of the gene.  
 Claim 1; SEQ ID NO 1; 79pp; English.  
 The invention relates to identifying an agent that modulates the activity of a cancer-related gene. The method involves contacting a compound with a cell containing a gene that corresponds to a polynucleotide having a sequence selected from (SEQ ID NO. 1-18) under conditions promoting the expression of the gene. The method is useful for identifying an agent that modulates the activity of a cancer-related gene. The polypeptides and antibodies of the invention are useful for treating and diagnosing cancer, preferably prostate cancer. It is also useful for screening assays for agents that are effective in reducing the activity of cancer-related genes. The present sequence represents a specific example of a cancer-related polynucleotide sequence.  
 Sequence 5271 BP; 1480 A; 1087 C; 1212 G; 1492 T; 0 U; 0 Other;  
 Query Match 99.9%; Score 3974.8; DB 12; Length 5271;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 ATGCTGCCCTGTACAGGAGGTCAAGCCCAACCCGCTGCAGGACGCAACCTCTGCTCA 60  
 Db 116 ATGCTGCCCTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCAACCTCTGCTCA 175  
 Qy 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAG 120  
 Db 176 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAG 235  
 Qy 121 GAGATGATATGATTTTCAAGTGTGTCAGAGAGACCGCTCAGACACCTTGGAGAGATTG 180  
 Db 236 GAGATGATATGATTTTCAAGTGTGTCAGAGAGACCGCTCAGACACCTTGGAGAGATTG 295  
 Qy 181 CAAGGTTCTCGGATAAAGAAAGTTTAAAGAGCTGAGAAATGAGCAAGAGCCCTTTT 240  
 Db 296 CAAGGTTCTCGGATAAAGAAAGTTTAAAGAGCTGAGAAATGAGCAAGAGCCCTTTT 355  
 Qy 241 ACAAGCAATCATAAAGTGTCTAGTGAATCTTATTTAGTTTGGAAATTTTACGTTA 300  
 Db 356 ACAAGCAATCATAAAGTGTCTAGTGAATCTTATTTAGTTTGGAAATTTTACGTTA 415  
 Qy 301 ATTGAGAAAGTGCAGAAAGTAAATCCAGCCCATATTTTGGGAAAAATATTAATTTT 360  
 Db 416 ATTGAGAAAGTGCAGAAAGTAAATCCAGCCCATATTTTGGGAAAAATATTAATTTT 475  
 Qy 361 GAAATTTATGATCCATGGATTTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 420  
 Db 476 GAAATTTATGATCCATGGATTTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 535  
 Qy 421 CTGACTTTTTCAGCGCTCAATTTTGGCTATATCTGCATCACTTATTTTATCAGTTTCA 480



QY 2641 TATTTTGGAAACGTCAGAGATGTGAAGCGCTGGAATCTCAAACTCGAGTCCAGTG 2700  
DB |||||||  
QY 2756 TATTTTGGAAACGTCAGAGATGTGAAGCGCTGGAATCTCAAACTCGAGTCCAGTG 2815  
DB |||||||  
QY 2701 TTTTCCCACTTGTCTCTCTCCAGGGCTCTGGACCATCCGGGATACAAAGCAGAA 2760  
DB |||||||  
QY 2816 TTTTCCCACTTGTCTCTCTCCAGGGCTCTGGACCATCCGGGATACAAAGCAGAA 2875  
DB |||||||  
QY 2761 GAGAGTGTGAGAACTGTGTGATGACACACAGATTTACATTCAGAGGCTTGTCTTG 2820  
DB |||||||  
QY 2876 GAGAGTGTGAGAACTGTGTGATGACACACAGATTTACATTCAGAGGCTTGTCTTG 2935  
DB |||||||  
QY 2821 TTTTGTGACAACTGCGCTGCTGCGCTGCTGCGATGCACTCTGCGATGCGGGCAGGTTGGT 2880  
DB |||||||  
QY 2936 TTTTGTGACAACTGCGCTGCTGCGCTGCTGCGATGCACTCTGCGATGCGGGCAGGTTGGT 2995  
DB |||||||  
QY 2881 ATCATCGTTGCTTGTGGTCCCTGATTTCTGGCAAAACTCTCTGGATGCGGGCAGGTTGGT 2940  
DB |||||||  
QY 2996 ATCATCGTTGCTTGTGGTCCCTGATTTCTGGCAAAACTCTCTGGATGCGGGCAGGTTGGT 3055  
DB |||||||  
QY 2941 TTGCACTGCTATGCTCTCACGCTCATGCGGATGTTTTCAGTGGTGTGTTGCAAAAGT 3000  
DB |||||||  
QY 3056 TTGCACTGCTATGCTCTCACGCTCATGCGGATGTTTTCAGTGGTGTGTTGCAAAAGT 3115  
DB |||||||  
QY 3001 GCTGAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3060  
DB |||||||  
QY 3116 GCTGAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3175  
DB |||||||  
QY 3061 AAAGAAGCACCCTTGGGAATATCAGAAACGCCACCACGAGCTGGCCCCCATGAGGAGTG 3120  
DB |||||||  
QY 3176 AAAGAAGCACCCTTGGGAATATCAGAAACGCCACCACGAGCTGGCCCCCATGAGGAGTG 3235  
DB |||||||  
QY 3121 ATAATCTTTGACAACTGAACTTCATGTACAGTCCAGTGGGCTCTGTTACTGCAAGCAT 3180  
DB |||||||  
QY 3236 ATAATCTTTGACAACTGAACTTCATGTACAGTCCAGTGGGCTCTGTTACTGCAAGCAT 3295  
DB |||||||  
QY 3181 CTGACAGCACTCAATTAATCACAAGAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
DB |||||||  
QY 3296 CTGACAGCACTCAATTAATCACAAGAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3355  
DB |||||||  
QY 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTTGTGAGAACCCGAGGTAAATTTGGATT 3300  
DB |||||||  
QY 3356 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTTGTGAGAACCCGAGGTAAATTTGGATT 3415  
DB |||||||  
QY 3301 GATTAAGATCTTGACAACTGAAATTTGACCTTCAAGTTAAGGAAGAAATGTCAATCAT 3360  
DB |||||||  
QY 3416 GATTAAGATCTTGACAACTGAAATTTGACCTTCAAGTTAAGGAAGAAATGTCAATCAT 3475  
DB |||||||  
QY 3361 CCTCAGGAACCTGTTTGTTCACCTGGAAACATGAGGAACCTGGATCCCTTTTAATGAG 3420  
DB |||||||  
QY 3476 CCTCAGGAACCTGTTTGTTCACCTGGAAACATGAGGAACCTGGATCCCTTTTAATGAG 3535  
DB |||||||  
QY 3421 CACAGGATGAGGAACCTGGAATGCTTCAAGAGGTACAACTTAAAGAAACCAATTGAA 3480  
DB |||||||  
QY 3536 CACAGGATGAGGAACCTGGAATGCTTCAAGAGGTACAACTTAAAGAAACCAATTGAA 3595  
DB |||||||  
QY 3481 GATCTTCTGTAAATGATGATGAACTAGCAGATCCAAATTTAGTGTGGA 3540  
DB |||||||  
QY 3596 GATCTTCTGTAAATGATGATGAACTAGCAGATCCAAATTTAGTGTGGA 3655  
DB |||||||  
QY 3541 CAAGAACAACCTGTTGCTTGGCAGGCAATCTCAGGAATAATCAGATATGATTTATT 3600  
DB |||||||  
QY 3656 CAAGAACAACCTGTTGCTTGGCAGGCAATCTCAGGAATAATCAGATATGATTTATT 3715  
DB |||||||  
QY 3601 GATGAAGCGAGGCAATGTGGATCCAGAACTGATGATGTTTAATACAAAAAATCCGG 3660  
DB |||||||  
QY 3716 GATGAAGCGAGGCAATGTGGATCCAGAACTGATGATGTTTAATACAAAAAATCCGG 3775  
DB |||||||  
QY 3661 GAGAAATTTGCCCACTGACCGTGTCAACGATTCGACACAGATTTGATTTAGAC 3720  
DB |||||||  
QY 3776 GAGAAATTTGCCCACTGACCGTGTCAACGATTCGACACAGATTTGATTTAGAC 3835  
DB |||||||  
QY 3721 AGCCACAAGATAATGGTTTTTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGCTATGTT 3780

DB 3836 AGCGACAAGATATGTTTAGATTAGAGAACTGAAAGATATGATGAGCCGATGTT 3895  
QY 3781 TTGCTGCAAAATAAAGAGAGCCTATTTTTCAAGATGTGCAACAACCTGGGCAAGGCAGAA 3840  
DB 3896 TTGCTGCAAAATAAAGAGAGCCTATTTTTCAAGATGTGCAACAACCTGGGCAAGGCAGAA 3955  
QY 3841 GCCGCTGCCCTCACTGAAACAGCAACAGGATACCTTCAAAAGAAATTTCCACATATT 3900  
DB 3956 GCCGCTGCCCTCACTGAAACAGCAACAGGATACCTTCAAAAGAAATTTCCACATATT 4015  
QY 3901 GGTCACACTGACCACTGTTTACAAACACATTTCAATGGACAGCCCTCGACATATT 3960  
DB 4016 GGTCACACTGACCACTGTTTACAAACACATTTCAATGGACAGCCCTCGACATATT 4075  
QY 3961 TTCGAGACAGCACTGTGA 3978  
DB 4076 TTCGAGACAGCACTGTGA 4093

RESULT 4  
ADH10612  
ID ADH10612 standard; DNA; 5284 BP.  
XX  
AC ADH10612;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
DE Human cancer-related polynucleotide, SEQ ID 2.  
XX  
KW Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2003104404-A2.  
XX  
PD 18-DEC-2003.  
XX  
PF 05-JUN-2003; 2003WO-US017772.  
XX  
PR 06-JUN-2002; 2002US-0386651P.  
XX  
XX (AVAL-) AVALON PHARM INC.  
XX  
PI Ebner R;  
XX  
XX WPI; 2004-062332/06.  
XX  
PT Identifying agents that modulate the activity of cancer-related gene,  
PT useful for treating or diagnosing prostate cancer comprising contacting a  
PT compound with a cell containing a gene under conditions promoting  
PT expression of the gene.  
XX  
XX Claim 1; SEQ ID NO 2; 79pp; English.  
XX  
CC The invention relates to identifying an agent that modulates the activity  
CC of a cancer-related gene. The method involves contacting a compound with  
CC a cell containing a gene that corresponds to a polynucleotide having a  
CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the  
CC expression of the gene. The method is useful for identifying an agent  
CC that modulates the activity of a cancer-related gene. The polypeptides  
CC and antibodies of the invention are useful for treating and diagnosing  
CC cancer, preferably prostate cancer. It is also useful for screening  
CC assays for agents that are effective in reducing the activity of cancer-  
CC related genes. The present sequence represents a specific example of a  
CC cancer-related polynucleotide sequence.

XX  
SQ Sequence 5284 BP; 1480 A; 1138 C; 1210 G; 1456 T; 0 U; 0 Other;

Query Match 99.9%; Score 3974.8; DB 12; Length 5284;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCTGCCCGTGTACAGAGGTTGAAGCCCAACCCGCTGCGAGGAGCGGAACTCTGCTCA 60  
 Db 116 ATGCTGCCCGTGTACAGAGGTTGAAGCCCAACCCGCTGCGAGGAGCGGAACTCTGCTCA 175  
 QY 61 CGCGTGTCTTCTGCTGGCTCAATCCCTGTTTAAATTTGGCCATAAAGCGAGATTAGAG 120  
 Db 176 CGCGTGTCTTCTGCTGGCTCAATCCCTGTTTAAATTTGGCCATAAAGCGAGATTAGAG 235  
 QY 121 GAAGATGATATGTATTCAGTGTCTGCGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG 180  
 Db 236 GAAGATGATATGTATTCAGTGTCTGCGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG 295  
 QY 181 CAAGGTTCTGGATAAAGAGTTTAAAGCTGAGATGAGATGAGACGACGCTTCTTTA 240  
 Db 296 CAAGGTTCTGGATAAAGAGTTTAAAGCTGAGATGAGATGAGACGACGCTTCTTTA 355  
 QY 241 ACAAGAGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
 Db 356 ACAAGAGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 415  
 QY 301 ATTGAGGAAAGTGCCAAAGTAAATCCAGGCCCATATTTTGGGAAATTTTAAATTTT 360  
 Db 416 ATTGAGGAAAGTGCCAAAGTAAATCCAGGCCCATATTTTGGGAAATTTTAAATTTT 475  
 QY 361 GAAATTTATGATCCCATGGATTCGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 420  
 Db 476 GAAATTTATGATCCCATGGATTCGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 535  
 QY 421 CTGACTTTTTCAGCGCTCATTTTGGCTATCTGCTATCTGATCACTTATTTTATCAGTTTCA 480  
 Db 536 CTGACTTTTTCAGCGCTCATTTTGGCTATCTGCTATCTGATCACTTATTTTATCAGTTTCA 595  
 QY 481 TGTCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACTTCGT 540  
 Db 596 TGTCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACTTCGT 655  
 QY 541 CTTAGTAAATGCGCATGGGGAAGAACACACAGGCCAGATGATCAATCTGCTGTCCAAT 600  
 Db 656 CTTAGTAAATGCGCATGGGGAAGAACACACAGGCCAGATGATCAATCTGCTGTCCAAT 715  
 QY 601 GATGTGAACAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGCGGAGGACCACTG 660  
 Db 716 GATGTGAACAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGCGGAGGACCACTG 775  
 QY 661 CAGCGGATCGCAGTGAATCTGCTGCTGAGTAGGAATATCGTGTCTGCTGGG 720  
 Db 776 CAGCGGATCGCAGTGAATCTGCTGCTGAGTAGGAATATCGTGTCTGCTGGG 835  
 QY 721 ATGCGAGTCTTAATCATTTCTCTGCTGCTGCAAGAGCTGTTTGGGAAAGTTGTTCTCATCA 780  
 Db 836 ATGCGAGTCTTAATCATTTCTCTGCTGCTGCAAGAGCTGTTTGGGAAAGTTGTTCTCATCA 895  
 QY 781 CTGAGGAGTAAATCTGCACTTTCAGGATGCGAGGATCAGGACCATGAATGAAGTTATA 840  
 Db 896 CTGAGGAGTAAATCTGCACTTTCAGGATGCGAGGATCAGGACCATGAATGAAGTTATA 955  
 QY 841 ACTGCTATAGGATAAATAAAGTGTACGCTGCGGAAAGTCAATTTTCAAATCTTATTAACC 900  
 Db 956 ACTGCTATAGGATAAATAAAGTGTACGCTGCGGAAAGTCAATTTTCAAATCTTATTAACC 1015  
 QY 901 AATTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAAGTTTCTGCTCAGGGGATGAAT 960  
 Db 1016 AATTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAAGTTTCTGCTCAGGGGATGAAT 1075  
 QY 961 TTGCTTCTGTTTTCAGTGCAGCAAAATCATCTGTTTGTGACCTTCAACCATCTAGCTG 1020  
 Db 1076 TTGCTTCTGTTTTCAGTGCAGCAAAATCATCTGTTTGTGACCTTCAACCATCTAGCTG 1135  
 QY 1021 CTCCTCGCGAGTGTATCACAGCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080  
 Db 1136 CTCCTCGCGAGTGTATCACAGCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195  
 QY 1081 GTGCGGCTGACGGTTACCCCTCTTCTTCCCTCAGCCATTGAGAGGGTGTTCAGAGGCAATC 1140

Db 1196 GTGCGGCTGACGGTTACCCCTTCTTCCCTCAGCCATTTGAGAGGGTGTTCAGAGCAATC 1255  
 QY 1141 GTGAGCATCCGAGAAATCCAGACCTTTTGTCTACTTGATGAGATATCACAGCGCAACCGT 1200  
 Db 1256 GTGAGCATCCGAGAAATCCAGACCTTTTGTCTACTTGATGAGATATCACAGCGCAACCGT 1315  
 QY 1201 CAGCTGCCGTGAGATGGTAAAGATGGTGCATGTGCAAGGATTTTACTGCTTTTGGGAT 1260  
 Db 1316 CAGCTGCCGTGAGATGGTAAAGATGGTGCATGTGCAAGGATTTTACTGCTTTTGGGAT 1375  
 QY 1261 AAGCATCAGAGACCCCACTCTACAGGCCCTTCTTCTTACTGTGACAGCCTGGCGAATTG 1320  
 Db 1376 AAGCATCAGAGACCCCACTCTACAGGCCCTTCTTCTTACTGTGACAGCCTGGCGAATTG 1435  
 QY 1321 TTAGCTGTGGTGGCGCCCGTGGGAGCAGGGAAGTCACTACCTGTTAAAGTGGCGTCTCGG 1380  
 Db 1436 TTAGCTGTGGTGGCGCCCGTGGGAGCAGGGAAGTCACTACCTGTTAAAGTGGCGTCTCGG 1495  
 QY 1381 GAATTGGCCCCAAGTCAAGGCTGCTGATGAGCGTGCATGGAGAAATTTGCCCTATGTCTCAG 1440  
 Db 1496 GAATTGGCCCCAAGTCAAGGCTGCTGATGAGCGTGCATGGAGAAATTTGCCCTATGTCTCAG 1555  
 QY 1441 CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATTTTATTTGGGAAAGAAATACGAA 1500  
 Db 1556 CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATTTTATTTGGGAAAGAAATATGAA 1615  
 QY 1501 AAGGAAAGATATGAAAGTCAAAAGCTGCTGCTCTGAAAAGGATTTACAGCTGTTG 1560  
 Db 1616 AAGGAAAGATATGAAAGTCAAAAGCTGCTGCTCTGAAAAGGATTTACAGCTGTTG 1675  
 QY 1561 GAGATGCTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAA 1620  
 Db 1676 GAGATGCTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAA 1735  
 QY 1621 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGATCATCTCTCTGAGCGAT 1680  
 Db 1736 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGATCATCTCTCTGAGCGAT 1795  
 QY 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
 Db 1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855  
 QY 1741 ATTTGATCAGAGAGATCAAAATTTTGTGACTCATCATGTTGCTGAGTACCTCAAGCTGCA 1800  
 Db 1856 ATTTGATCAGAGAGATCAAAATTTTGTGACTCATCATGTTGCTGAGTACCTCAAGCTGCA 1915  
 QY 1801 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGTGTGCAAGGCGACTTACACTGAGTTC 1860  
 Db 1916 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGTGTGCAAGGCGACTTACACTGAGTTC 1975  
 QY 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAA 1920  
 Db 1976 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAA 2035  
 QY 1921 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGTTTGG 1980  
 Db 2036 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGTTTGG 2095  
 QY 1981 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTGTCTCTGGAGAGCCAAAGATACAGAG 2040  
 Db 2096 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTGTCTCTGGAGAGCCAAAGATACAGAG 2155  
 QY 2041 AATGTCCAGTTACACTATCAGAGGAAACCGTTCTGAAGAAAGTGGTTTTCAGGCC 2100  
 Db 2156 AATGTCCAGTTACACTATCAGAGGAAACCGTTCTGAAGAAAGTGGTTTTCAGGCC 2215  
 QY 2101 TATAAGAAATTTACTTTCAGAGCTGGTGTCTACCTGGATTGTCTTCAATTTTCTTATCTCTTA 2160  
 Db 2216 TATAAGAAATTTACTTTCAGAGCTGGTGTCTACCTGGATTGTCTTCAATTTTCTTATCTCTTA 2275  
 QY 2161 AACACTGACGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTCATATCTGGGCAATC 2220

D	b	2276	AACACTGAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTTCATACTGGGCAAC	2335
Q	y	2221	AAACAAAGTATGCTAAATGTCACCTGTAAATGGAGGAGGAAATGTAAACCGAGAAGCTAGAT	2280
D	b	2336	AAACAAAGTATGCTAAATGTCACCTGTAAATGGAGGAGGAAATGTAAACCGAGAAGCTAGAT	2395
Q	y	2281	CTTAACCTGGTACTTATAGGAATTTATTTACAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA	2340
D	b	2396	CTTAACCTGGTACTTATAGGAATTTATTTACAGGTTTAACTGTAGCTACCGTTCCTTTTGGCATA	2455
Q	y	2341	GCAAGATCTCTATTGGTATTCTACGTCCTTGTAACTCTTTCACAAACTTTGCAACAACAA	2400
D	b	2456	GCAAGATCTCTATTGGTATTCTACGTCCTTGTAACTCTTTCACAAACTTTGCAACAACAA	2515
Q	y	2401	ATGTTTGAGTCAATCTGAAAGCTCCGGTATATTCTTTGATAGAAATCCATAGGAAGA	2460
D	b	2516	ATGTTTGAGTCAATCTGAAAGCTCCGGTATATTCTTTGATAGAAATCCATAGGAAGA	2575
Q	y	2461	ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT	2520
D	b	2576	ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT	2635
Q	y	2521	TTAGATTTCATCCAGACATTGCTACAAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG	2580
D	b	2636	TTAGATTTCATCCAGACATTGCTACAAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG	2695
Q	y	2581	ATTCCTTGGATCGCAATACCTTGGTTCCTTGGTTCCTTGGAAATCAATTTTCATTTTCTCGGCGA	2640
D	b	2696	ATTCCTTGGATCGCAATACCTTGGTTCCTTGGTTCCTTGGAAATCAATTTTCATTTTCTCGGCGA	2755
Q	y	2641	TATTTTGGAAACGTCACAGAGATGTCGAAGCGCTGGAATCTACAACTCCGAGTCCAGTG	2700
D	b	2756	TATTTTGGAAACGTCACAGAGATGTCGAAGCGCTGGAATCTACAACTCCGAGTCCAGTG	2815
Q	y	2701	TTTTTCCCACTTGTCACTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2760
D	b	2816	TTTTTCCCACTTGTCACTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2875
Q	y	2761	GAGAGGTGTACGAACTGTGTTGATGACACACAGATTTACATTCAGAGGCTTGGTCTTGT	2820
D	b	2876	GAGAGGTGTACGAACTGTGTTGATGACACACAGATTTACATTCAGAGGCTTGGTCTTGT	2935
Q	y	2821	TTTTTTGACAAACGTCGCGTGGTTCGCGTCTGGATGCCATCTGTGCCATGTTTGTG	2880
D	b	2936	TTTTTTGACAAACGTCGCGTGGTTCGCGTCTGGATGCCATCTGTGCCATGTTTGTG	2995
Q	y	2881	ATCATCGTTGCTTGGGTCCCTGATTTCTGGCAAAACCTCTGGATGCCGGCAGGTTGGT	2940
D	b	2996	ATCATCGTTGCTTGGGTCCCTGATTTCTGGCAAAACCTCTGGATGCCGGCAGGTTGGT	3055
Q	y	2941	TTGGCACTGCTTATGCCCTCACGCTCATGCGGATGTTTCAGTGGTGTGTTTCGACAAAGT	3000
D	b	3056	TTGGCACTGCTTATGCCCTCACGCTCATGCGGATGTTTCAGTGGTGTGTTTCGACAAAGT	3115
Q	y	3001	GCTCAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACTTTGAA	3060
D	b	3116	GCTCAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACTTTGAA	3175
Q	y	3061	AAAGAAGCACCTTGGGAATATCAGAAACGCCACACACAGCGCTGGCCCCCATGAAGGAGTG	3120
D	b	3176	AAAGAAGCACCTTGGGAATATCAGAAACGCCACACACAGCGCTGGCCCCCATGAAGGAGTG	3235
Q	y	3121	ATAATCTTTGACAAATGTAATCTCATGTACAGTCCAGTGGGCTCTGGTACTGAAGCAT	3180
D	b	3236	ATAATCTTTGACAAATGTAATCTCATGTACAGTCCAGTGGGCTCTGGTACTGAAGCAT	3295
Q	y	3181	CTGACAGCACTCATTAATACAAAGAAAGGTTGSCATTTGGGAAGAACCGGAGCTGGA	3240
D	b	3296	CTGACAGCACTCATTAATACAAAGAAAGGTTGSCATTTGGGAAGAACCGGAGCTGGA	3355
Q	y	3241	AAAAAGTTCCCTCATCTCAGCCCTTTTTTAGATTGTGACAAACCGAAGGTAAATTTGGATT	3300
D	b	3356	AAAAAGTTCCCTCATCTCAGCCCTTTTTTAGATTGTGACAAACCGAAGGTAAATTTGGATT	3415

Q	y	3301	GATAAGATCTTGACAACTGAAATTTGGACTTTCAGATTTTAAGGAGGAAATGTCATCATATA	3360
D	b	3416	GATAAGATCTTGACAACTGAAATTTGGACTTTCAGATTTTAAGGAGGAAATGTCATCATATA	3475
Q	y	3361	CCTCAGGAACTCTGTTTGTGTTTCACTGGAAACAATGAGGAAAAACCTGGATCCCTTTAATGAG	3420
D	b	3476	CCTCAGGAACTCTGTTTGTGTTTCACTGGAAACAATGAGGAAAAACCTGGATCCCTTTAATGAG	3535
Q	y	3421	CACACGATGAGGAACTGTGTGAATGCTTTCAGAGGTACAACCTTAAGAAAAACCATTTGAA	3480
D	b	3536	CACACGATGAGGAACTGTGTGAATGCTTTCAGAGGTACAACCTTAAGAAAAACCATTTGAA	3595
Q	y	3481	GATCTTCTCGTAAATGATGATCTGATTTAGCAGAATCAGATCCCAATTTTAGTGTGGGA	3540
D	b	3596	GATCTTCTCGTAAATGATGATCTGATTTAGCAGAATCAGATCCCAATTTTAGTGTGGGA	3655
Q	y	3541	CAAAAGCAACTGGTGTGCTTGGCAGGCAATTTCTCAGGAAAAATCAGATATTGATTATT	3600
D	b	3656	CAAAAGCAACTGGTGTGCTTGGCAGGCAATTTCTCAGGAAAAATCAGATATTGATTATT	3715
Q	y	3601	GATGAACGACGCGCAATGTGGATCCAAAGAACTGATGAGTTTAATACAAAAAATAATCCGG	3660
D	b	3716	GATGAACGACGCGCAATGTGGATCCAAAGAACTGATGAGTTTAATACAAAAAATAATCCGG	3775
Q	y	3661	GAGAAATTTGCCCACTGCACCGTCTAAACCATTTGCACACAGATTTGAACCATTTATTGAC	3720
D	b	3776	GAGAAATTTGCCCACTGCACCGTCTAAACCATTTGCACACAGATTTGAACCATTTATTGAC	3835
Q	y	3721	AGGCACAAGATAATGTTTTAGATTTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT	3780
D	b	3836	AGGCACAAGATAATGTTTTAGATTTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT	3895
Q	y	3781	TTGCTGCAAAATAAAGAGAGCCTATTTTTACAAGATGTGCAACAACTGGGCAAGGCGAGAA	3840
D	b	3896	TTGCTGCAAAATAAAGAGAGCCTATTTTTACAAGATGTGCAACAACTGGGCAAGGCGAGAA	3955
Q	y	3841	GCCGCTGCCCTCACTGAAACAGCAAGAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT	3900
D	b	3956	GCCGCTGCCCTCACTGAAACAGCAAGAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT	4015
Q	y	3901	GGTCACACTGACCACTGGTTTACAAACACTTTCCAATGGACAGCCCTCGACCTTAACATT	3960
D	b	4016	GGTCACACTGACCACTGGTTTACAAACACTTTCCAATGGACAGCCCTCGACCTTAACATT	4075
Q	y	3961	TTGAGAGACAGCACTGTGA 3978	
D	b	4076	TTGAGAGACAGCACTGTGA 4093	

## RESULT 5

ADH10624  
ID ADH10624 standard; DNA; 5833 BP.

XX ADH10624;

XX 11-MAR-2004 (first entry)

XX Human cancer-related polynucleotide, SEQ ID 14.

XX Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.

XX Homo sapiens.

XX WO2003104404-A2.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-US017772.

XX 06-JUN-2002; 2002US-0386651P.

XX (AVAL-) AVALON PHARM INC.

XX Ebner R;  
XX PI  
XX DR WPI; 2004-062332/06.  
XX  
XX Identifying agents that modulate the activity of cancer-related gene,  
XX useful for treating or diagnosing prostate cancer comprising contacting a  
XX compound with a cell containing a gene under conditions promoting a  
XX expression of the gene.  
XX  
XX Claim 1; SEQ ID NO 14; 79pp; English.  
XX  
XX The invention relates to identifying an agent that modulates the activity  
XX of a cancer-related gene. The method involves contacting a compound with  
XX a cell containing a gene that corresponds to a polynucleotide having a  
XX sequence selected from (SEQ ID NO. 1-18) under conditions promoting the  
XX expression of the gene. The method is useful for identifying an agent  
XX that modulates the activity of a cancer-related gene. The polypeptides  
XX and antibodies of the invention are useful for treating and diagnosing  
XX cancer, preferably prostate cancer. It is also useful for screening  
XX assays for agents that are effective in reducing the activity of cancer-  
XX related genes. The present sequence represents a specific example of a  
XX cancer-related polynucleotide sequence.  
XX  
SQ Sequence 5833 BP; 1660 A; 1175 C; 1306 G; 1692 T; 0 U; 0 Other;  
  
Query Match 99.9%; Score 3974.8; DB 12; Length 5833;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 ATGCTGCCGTGTACAGAGGTGAAGCCCAACCGCTGCGAGGACGGAACTCTGCTCA 60  
Db 116 ATGCTGCCGTGTACAGAGGTGAAGCCCAACCGCTGCGAGGACGGAACTCTGCTCA 175  
  
Qy 61 GCGGTGCTCTCTGGTGGCTCAATCCCTGTTTAAATTTGGCCATAAATCGGAGATTAG 120  
Db 176 GCGGTGCTCTCTGGTGGCTCAATCCCTGTTTAAATTTGGCCATAAATCGGAGATTAG 235  
  
Qy 121 GAAGATGATATGATTCAGTCTGCGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG 180  
Db 236 GAAGATGATATGATTCAGTCTGCGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG 295  
  
Qy 181 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATGACGACAGAACCTTCTTTA 240  
Db 296 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATGACGACAGAACCTTCTTTA 355  
  
Qy 241 ACAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
Db 356 ACAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 415  
  
Qy 301 ATTGAGAAAGTGCAGAAATTAATCCAGCCCATATTTTGGGAAATTTTATTAATTTT 360  
Db 416 ATTGAGAAAGTGCAGAAATTAATCCAGCCCATATTTTGGGAAATTTTATTAATTTT 475  
  
Qy 361 GAAATATTATGATCCCATGATTTCTGGCTTTTGAACACAGCGTACGCTATGCCACGGTG 420  
Db 476 GAAATATTATGATCCCATGATTTCTGGCTTTTGAACACAGCGTACGCTATGCCACGGTG 535  
  
Qy 421 CTGACTTTTTCAGCGCTCAATTTGGCTATCTGATCATCTATATTTTATCAGTTTCAG 480  
Db 536 CTGACTTTTTCAGCGCTCAATTTGGCTATCTGATCATCTATATTTTATCAGTTTCAG 595  
  
Qy 481 TGTCTGGGATGAGTTACGATGAGCATGTCATATTTATCGGAGGCACTTCGT 540  
Db 596 TGTCTGGGATGAGTTACGATGAGCATGTCATATTTATCGGAGGCACTTCGT 655  
  
Qy 541 CTTAGTAACATGGCCATGGGGAAGAACCAACAGCCAGATAGTCAATCTCTGTCCTCAAT 600  
Db 656 CTTAGTAACATGGCCATGGGGAAGAACCAACAGCCAGATAGTCAATCTCTGTCCTCAAT 715  
  
Qy 601 GATGTGAACAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGACGAGCACTG 660  
Db 716 GATGTGAACAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGACGAGCACTG 775

Qy 661 CAGCGCATCGCAGTGAATGCGCTTACTCTGGATGAGATAGGAATATCGTGCCTTCTCGG 720  
Db 776 CAGCGCATCGCAGTGAATGCGCTTACTCTGGATGAGATAGGAATATCGTGCCTTCTCGG 835  
  
Qy 721 ATGGCAGTTCTAAATCAATCTCTGCCCTTGAAGAGCTGTTTGGGAAGTGTCTTCATCA 780  
Db 836 ATGGCAGTTCTAAATCAATCTCTGCCCTTGAAGAGCTGTTTGGGAAGTGTCTTCATCA 895  
  
Qy 781 CTGAGGAGTAAACCTGCAACTTTTCCAGATGCCAGATCAGGACCATCAATGAAGTTATA 840  
Db 896 CTGAGGAGTAAACCTGCAACTTTTCCAGATGCCAGATCAGGACCATCAATGAAGTTATA 955  
  
Qy 841 ACTGGTATAAGGATAAATAAATGATGCGCTTGGGAAAGTCAATTTCAAATCTTATTACC 900  
Db 956 ACTGGTATAAGGATAAATAAATGATGCGCTTGGGAAAGTCAATTTCAAATCTTATTACC 1015  
  
Qy 901 AATTGAGAAAGAGGAGATTTCAGAGATTCAGAGATTCCTGCTCAGGGGAGATGAAT 960  
Db 1016 AATTGAGAAAGAGGAGATTTCAGAGATTCAGAGATTCCTGCTCAGGGGAGATGAAT 1075  
  
Qy 961 TTGGCTTCTGTTTTCAGTGAAGCAAAATCATCGTGTGAGCTTCCACCATCTACCTG 1020  
Db 1076 TTGGCTTCTGTTTTCAGTGAAGCAAAATCATCGTGTGAGCTTCCACCATCTACCTG 1135  
  
Qy 1021 CTCCTCGCAGTGTGATCACAGCCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080  
Db 1136 CTCCTCGCAGTGTGATCACAGCCAGCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195  
  
Qy 1081 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGGTGTGAGAGCAATC 1140  
Db 1196 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGGTGTGAGAGCAATC 1255  
  
Qy 1141 GTGAGCATCGAAGATCCAGACCTTTTGTCTACTGATGAGATATCACAGCGCAACCGT 1200  
Db 1256 GTGAGCATCGAAGATCCAGACCTTTTGTCTACTGATGAGATATCACAGCGCAACCGT 1315  
  
Qy 1201 CAGCTGCCGTGAGATGTTAAAGATGTTGATGTCAGGAGATTTTACTGCTTTTGGGAT 1260  
Db 1316 CAGCTGCCGTGAGATGTTAAAGATGTTGATGTCAGGAGATTTTACTGCTTTTGGGAT 1375  
  
Qy 1261 AAGCATCAGAGACCCCAACTCTAACAGGCTTTTCTTTACTGTCAGACCTGGGGAATG 1320  
Db 1376 AAGCATCAGAGACCCCAACTCTAACAGGCTTTTCTTTACTGTCAGACCTGGGGAATG 1435  
  
Qy 1321 TTAGCTGTGCTCGCCCGCTGGGAGCAGGAGTATCATCTGTTAAGTGGCTGCTCGGG 1380  
Db 1436 TTAGCTGTGCTCGCCCGCTGGGAGCAGGAGTATCATCTGTTAAGTGGCTGCTCGGG 1495  
  
Qy 1381 GAATTTGGCCCCAAGTCAAGGCTGCTGATGTCAGGAGTATGCGGAAATTTGCTGTCTCAG 1440  
Db 1496 GAATTTGGCCCCAAGTCAAGGCTGCTGATGTCAGGAGTATGCGGAAATTTGCTGTCTCAG 1555  
  
Qy 1441 CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAAATTTTATTTGGGAAGAAATACGAA 1500  
Db 1556 CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAAATTTTATTTGGGAAGAAATACGAA 1615  
  
Qy 1501 AAGGAACGATATGAAAGAGTCAATAAGGCTTGTCTCTGAAAAGGATTTACAGCTGTTG 1560  
Db 1616 AAGGAACGATATGAAAGAGTCAATAAGGCTTGTCTCTGAAAAGGATTTTACAGCTGTTG 1675  
  
Qy 1561 GAGGATGCTGATCTGATGATAGGAGATCGGGGAAACCGCTGAGTGGAGGGCAGAAA 1620  
Db 1676 GAGGATGCTGATCTGATGATAGGAGATCGGGGAAACCGCTGAGTGGAGGGCAGAAA 1735  
  
Qy 1621 GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATCTGACATCTATCTCTCGGACGAT 1680  
Db 1736 GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATCTGACATCTATCTCTCGGACGAT 1795  
  
Qy 1681 CCTCTCAGTGCAGTATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA 1740  
Db 1796 CCTCTCAGTGCAGTATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA 1855



QY 1741 ATTTTGATGAGAGATCACAAATTTTAGTGACTCATCAGTTGCGAGTACCTCAGAGCTGCA 1800  
DB 1856 ATTTTGATGAGAGATCACAAATTTTAGTGACTCATCAGTTGCGAGTACCTCAAAGCTGCA 1915  
QY 1801 AGTCAGATTTCTGATATTTGAAAGATGGTAATAATGCTGCAGAGGGGACTTACACTGAGTTC 1860  
DB 1916 AGTCAGATTTCTGATATTTGAAAGATGGTAATAATGCTGCAGAGGGGACTTACACTGAGTTC 1975  
QY 1861 CTAAATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGAGAAAGTGAACAA 1920  
DB 1976 CTAAATCTCGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGAGAAAGTGAACAA 2035  
QY 1921 CCTCCAGTCCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGSGTTGG 1980  
DB 2036 CCTCCAGTCCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGSGTTGG 2095  
QY 1981 TCTCAACAATCTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2040  
DB 2096 TCTCAACAATCTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2155  
QY 2041 AATGTCCAGTTACACTATCAGAGAGAAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2100  
DB 2156 AATGTCCAGTTACACTATCAGAGAGAAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2215  
QY 2101 TATAAGAAATTAATTCAGAGCTGGTCTCAGTGAATGCTCTCATTTTCTTATTTCTCCTA 2160  
DB 2216 TATAAGAAATTAATTCAGAGCTGGTCTCAGTGAATGCTCTCATTTTCTTATTTCTCCTA 2275  
QY 2161 AACACTGCAGTCAAGTTGCTATGCTCTCAAGATTTGGTGGCTTTCATCTCGGGCAAC 2220  
DB 2276 AACACTGCAGTCAAGTTGCTATGCTCTCAAGATTTGGTGGCTTTCATCTCGGGCAAC 2335  
QY 2221 AAACAAAGTATGCTAAATGTCATCTGTAATGGAGAGGAAATGTAACCGAGAAGCTAGAT 2280  
DB 2336 AAACAAAGTATGCTAAATGTCATCTGTAATGGAGAGGAAATGTAACCGAGAAGCTAGAT 2395  
QY 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACGCTCTTTTGGCATA 2340  
DB 2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACGCTCTTTTGGCATA 2455  
QY 2341 GCAAGATCTCTATTTGGTATTTCTAGTCTCTGTTAACTCTTCACAAAATTTTGCAACAAA 2400  
DB 2456 GCAAGATCTCTATTTGGTATTTCTAGTCTCTGTTAACTCTTCACAAAATTTTGCAACAAA 2515  
QY 2401 ATGTTTGAGTCAATCTGAAAGCTCCGGTATTTATCTTTGTATAGAAATCCAATAGGAAGA 2460  
DB 2516 ATGTTTGAGTCAATCTGAAAGCTCCGGTATTTATCTTTGTATAGAAATCCAATAGGAAGA 2575  
QY 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCCGCTGACGTTT 2520  
DB 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCCGCTGACGTTT 2635  
QY 2521 TTAGATTTTCATCCAGACATTTCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGCTG 2580  
DB 2636 TTAGATTTTCATCCAGACATTTCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGCTG 2695  
QY 2581 ATTCTTTGATGCAATACCTTGGTTCCTTGGATTCATTTTCATTTTCTTCGCGGA 2640  
DB 2696 ATTCTTTGATGCAATACCTTGGTTCCTTGGATTCATTTTCATTTTCTTCGCGGA 2755  
QY 2641 TATTTTGGAAACGTCNAGAGATGTGNAAGCGCTGGAACTCAAACTCGGAGTCCAGTG 2700  
DB 2756 TATTTTGGAAACGTCNAGAGATGTGNAAGCGCTGGAACTCAAACTCGGAGTCCAGTG 2815  
QY 2701 TTTTCCCACTGTCTATCTTCTCCAGGGGCTCTGGACCATCCGGGCAATACAAAGCAGAA 2760  
DB 2816 TTTTCCCACTGTCTATCTTCTCCAGGGGCTCTGGACCATCCGGGCAATACAAAGCAGAA 2875  
QY 2761 GAGAGGTGTCAAGAACTGTTTGTATGCAACACAGGATTTTACATTCAGAGGCTTGTCTTG 2820  
DB 2876 GAGAGGTGTCAAGAACTGTTTGTATGCAACACAGGATTTTACATTCAGAGGCTTGTCTTG 2935  
QY 2821 TTTTGGACAAAGTCCCGCTGGTTCGCGCTCGTCTGGATGCCATCTGTGCCATGTTTGTG 2880

DB 2936 TTTTGGACAAAGTCCCGCTGGTTCGCGCTCGTCTGATGCCATCTGTGCCATGTTTGTG 2995  
QY 2881 ATCATCTTCCCTTTGGGTCCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT 2940  
DB 2996 ATCATCTTCCCTTTGGGTCCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT 3055  
QY 2941 TTGGCACTGTCTATGCTCCCTCAGCTCATCGGGAGTGTTCAGTGGTGTCTTCGACAAAGT 3000  
DB 3056 TTGGCACTGTCTATGCTCCCTCAGCTCATCGGGAGTGTTCAGTGGTGTCTTCGACAAAGT 3115  
QY 3001 GCTGAAGTCTCAGAAATATGATGATCTCAGTAGAAAGGCTCATTTGAATACACAGACTTTGAA 3060  
DB 3116 GCTGAAGTCTCAGAAATATGATGATCTCAGTAGAAAGGCTCATTTGAATACACAGACTTTGAA 3175  
QY 3061 AAAGAACGACCTTTGGGAATATCAGAAACGCCACCCACAGCTGGCCCCATGAAAGAGTG 3120  
DB 3176 AAAGAACGACCTTTGGGAATATCAGAAACGCCACCCACAGCTGGCCCCATGAAAGAGTG 3235  
QY 3121 ATAATCTTTGACAAATGTGAATCTCATGTCAGTCCAGGTGGGCTCTGTGACTGAAGCAT 3180  
DB 3236 ATAATCTTTGACAAATGTGAATCTCATGTCAGTCCAGGTGGGCTCTGTGACTGAAGCAT 3295  
QY 3181 CTGACAGACTCTCATTTAAATCAAGAAAGAGTGGCATTTGGGAAGAAACCGGAGCTGGA 3240  
DB 3296 CTGACAGACTCTCATTTAAATCAAGAAAGAGTGGCATTTGGGAAGAAACCGGAGCTGGA 3355  
QY 3241 AAAAGTTCCTCATCTCAGCCCTTTTGTAGATTTGTAGAACCCGAGGTAATAATTTGGAT 3300  
DB 3356 AAAAGTTCCTCATCTCAGCCCTTTTGTAGATTTGTAGAACCCGAGGTAATAATTTGGAT 3415  
QY 3301 GATAAGATCTTGACAACTGAATTTGACCTTTCAGATTTAAGGAAGAAATGTCATCATATA 3360  
DB 3416 GATAAGATCTTGACAACTGAATTTGACCTTTCAGATTTAAGGAAGAAATGTCATCATATA 3475  
QY 3361 CCTCAGGAACTGTGTTTGTCTCAGTGAACCAATGAGGAAACCTCTGGATCCCTTTAAATGAG 3420  
DB 3476 CCTCAGGAACTGTGTTTGTCTCAGTGAACCAATGAGGAAACCTCTGGATCCCTTTAAATGAG 3535  
QY 3421 CACACGGATGAGGAACCTGTGGAATGCTTACAAGAGTACAACCTTAAAGAAACCATTTGAA 3480  
DB 3536 CACACGGATGAGGAACCTGTGGAATGCTTACAAGAGTACAACCTTAAAGAAACCATTTGAA 3595  
QY 3481 GATCTTCTCGTAAATGATACCTGAATTTAGCAGAAATCAGATCCCAATTTTAGTGTGGA 3540  
DB 3596 GATCTTCTCGTAAATGATACCTGAATTTAGCAGAAATCAGATCCCAATTTTAGTGTGGA 3655  
QY 3541 CAAAGACAACTGGTGTGCTTGCAGGGCAATCTCAGGAAATTCAGATAATTCAGATTTATTT 3600  
DB 3656 CAAAGACAACTGGTGTGCTTGCAGGGCAATCTCAGGAAATTCAGATAATTCAGATTTATTT 3715  
QY 3601 GATGAACGCAACGGAATGTGGAATCCCAAGAACCTGATGAGTTAATACAAAAAATCCGG 3660  
DB 3716 GATGAACGCAACGGAATGTGGAATCCCAAGAACCTGATGAGTTAATACAAAAAATCCGG 3775  
QY 3661 GAGAAATTTGCCCACTGCAACGGTCTTAAACATTTGCAACAGATTTGAACCATTTATTTGAC 3720  
DB 3776 GAGAAATTTGCCCACTGCAACGGTCTTAAACATTTGCAACAGATTTGAACCATTTATTTGAC 3835  
QY 3721 AGCGACAAGATTAATGTTTGTAGATTTAGGAAAGACTGAAAGAAATATGATGAGCCGTATGTT 3780  
DB 3836 AGCGACAAGATTAATGTTTGTAGATTTAGGAAAGACTGAAAGAAATATGATGAGCCGTATGTT 3895  
QY 3781 TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGTGCAACCACTGGGCAAGGCAAGAA 3840  
DB 3896 TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGTGCAACCACTGGGCAAGGCAAGAA 3955  
QY 3841 GCCGCTGCCCTCACTGAAAACGCAAAACAGGTATCTTCAAAAGAAATTTATCCACATATT 3900  
DB 3956 GCCGCTGCCCTCACTGAAAACGCAAAACAGGTATCTTCAAAAGAAATTTATCCACATATT 4015  
QY 3901 GGTCACTGACCACTGGTTTACAAAACATTTCCAATGGAACAGCCCTCGACCTTAACTATT 3960



Db	4016	GGTCACTGACCATGGTTACAAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT	4075
Qy	3961	TTCGAGACGACACTGTGA	3978
Db	4076	TTCGAGACGACACTGTGA	4093
RESULT 6			
ADH10626	ID	ADH10626 standard; DNA; 5862 BP.	
XX	AC	ADH10626;	
XX	AC		
DT	11-MAR-2004	(first entry)	
XX	XX		
DE	Human cancer-related polynucleotide, SEQ ID 16.		
XX	XX		
KW	Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.		
XX	OS	Homo sapiens.	
XX	XX		
FN	WO2003104404-A2.		
XX	XX		
PD	18-DEC-2003.		
XX	XX		
PF	05-JUN-2003; 2003WO-US017772.		
XX	XX		
PR	06-JUN-2002; 2002US-0386651P.		
XX	XX		
PA	(AVAL-) AVALON PHARM INC.		
XX	XX		
PI	Ebner R;		
XX	XX		
DR	WPI; 2004-062332/06.		
XX	XX		
PT	Identifying agents that modulate the activity of cancer-related gene,		
PT	useful for treating or diagnosing prostate cancer comprising contacting a		
PT	compound with a cell containing a gene under conditions promoting		
PT	expression of the gene.		
XX	XX		
PS	Claim 1; SEQ ID NO 16; 79pp; English.		
XX	XX		
CC	The invention relates to identifying an agent that modulates the activity		
CC	of a cancer-related gene. The method involves contacting a compound with		
CC	a cell containing a gene that corresponds to a polynucleotide having a		
CC	sequence selected from (SEQ ID NO. 1-18) under conditions promoting the		
CC	expression of the gene. The method is useful for identifying an agent		
CC	that modulates the activity of a cancer-related gene. The polypeptides		
CC	and antibodies of the invention are useful for treating and diagnosing		
CC	cancer, preferably prostate cancer. It is also useful for screening		
CC	assays for agents that are effective in reducing the activity of cancer-		
CC	related genes. The present sequence represents a specific example of a		
CC	cancer-related polynucleotide sequence.		
XX	XX		
SQ	Sequence 5862 BP; 1645 A; 1208 C; 1328 G; 1681 T; 0 U; 0 Other;		
Query Match 99.9%; Score 3974.8; DB 12; Length 5862;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 3976; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	ATGCTGCCCGTGATACAGAGGTTGAAGCCCAACCCGCTGCAGGACGGAACCTCTGTCTCA	60
Db	116	ATGCTGCCCGTGATACAGAGGTTGAAGCCCAACCCGCTGCAGGACGGAACCTCTGTCTCA	175
Qy	61	CGCGTGTTCTTCGGTGGCTCATCCCTGTTTAAATTCGCCATAACCGAGATTAG	120
Db	176	CGCGTGTTCTTCGGTGGCTCAATCCCTGTTTAAATTCGCCATAACCGAGATTAG	235
Qy	121	GAAGATGATATGTATTCAAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG	180
Db	236	GAAGATGATATGTATTCAAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG	295
Qy	181	CAAGGGTTCTGGGATAAAGAAGTTTTTAAGAGCTGAGAATACCGCACAGAAGCCCTCTTTTA	240

Db	296		CAAGGGTCTCGGGATAAGAAGTTTTAAGAGCTGAGAAATGACGCACAGAAAGCCCTCTCTTA	355
Qy	241		ACAAGGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGAAATTTTTTACGTGA	300
Db	356		ACAAGGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGAAATTTTTTACGTGA	415
Qy	301		ATTGAGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTAATAATATTTT	360
Db	416		ATTGAGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTAATAATATTTT	475
Qy	361		GAATAATTGATCCCATGGAATCTGTGGCTTTGAAACACAGCGTAGCGCTATGCCAGGTG	420
Db	476		GAATAATTGATCCCATGGAATCTGTGGCTTTGAAACACAGCGTAGCGCTATGCCAGGTG	535
Qy	421		CTGACTTTTTGACGCTCATTTTTGGCTATACTGCATCACTTATTTTTTATCAGTTTCAG	480
Db	536		CTGACTTTTTGACGCTCATTTTTGGCTATACTGCATCACTTATTTTTTATCAGTTTCAG	595
Qy	481		TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTTCTG	540
Db	596		TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTTCTG	655
Qy	541		CTTAGTAACATGCCATGGGGAAGACAACACAGGCCAGATAGTCAATCTGCTGTCCAAT	600
Db	656		CTTAGTAACATGCCATGGGGAAGACAACACAGGCCAGATAGTCAATCTGCTGTCCAAT	715
Qy	601		GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGAGGACACACTG	660
Db	716		GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGAGGACACACTG	775
Qy	661		CAGGCGATCGAGTGAATGCGCTTACTGAGTAGGATAGGAATATCGTGCCCTGCTGGG	720
Db	776		CAGGCGATCGAGTGAATGCGCTTACTGAGTAGGATAGGAATATCGTGCCCTGCTGGG	835
Qy	721		ATGGCAGTTCTAATCAATCTCTGCGCCCTTGCAAGCTGTTTTGGGAAGTTGTTCTCATCA	780
Db	836		ATGGCAGTTCTAATCAATCTCTGCGCCCTTGCAAGCTGTTTTGGGAAGTTGTTCTCATCA	895
Qy	781		CTGAGAGTAAAACTGCACTTTACGGATGCCAGATCAGGACCATGAATGAAGTTATA	840
Db	896		CTGAGAGTAAAACTGCACTTTACGGATGCCAGATCAGGACCATGAATGAAGTTATA	955
Qy	841		ACTGGTAAAGGATAAATAAAATGTAGCGCTGGGAAAAGTCATTTTCAAATCTTATACC	900
Db	956		ACTGGTAAAGGATAAATAAAATGTAGCGCTGGGAAAAGTCATTTTCAAATCTTATACC	1015
Qy	901		AATTTGAGAAAGAGGATTTTCAAAGTTCTGAGAAGTTCTGCTCTCAGGGGGATGAAT	960
Db	1016		AATTTGAGAAAGAGGATTTTCAAAGTTCTGAGAAGTTCTGCTCTCAGGGGGATGAAT	1075
Qy	961		TTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTGTCACCTTCCACCTACGCTG	1020
Db	1076		TTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTGTCACCTTCCACCTACGCTG	1135
Qy	1021		CTCCTCGGAGTGTGATCAAGCAGCCCGGTGTTCTGGCGAGTGAAGTGTATGGGGCT	1080
Db	1136		CTCCTCGGAGTGTGATCAAGCAGCCCGGTGTTCTGGCGAGTGAAGTGTATGGGGCT	1195
Qy	1081		GTGCGGTGACGGTTACCTTCTTCCCTCAGCCATTTGAGAGGGGTGCAGAGGCAATC	1140
Db	1196		GTGCGGTGACGGTTACCTTCTTCCCTCAGCCATTTGAGAGGGGTGCAGAGGCAATC	1255
Qy	1141		GTGAGCATCCGAGAAATCCAGACTTTTTGCTACTTGTATGAGATATCACAGCGCAACCGT	1200
Db	1256		GTGAGCATCCGAGAAATCCAGACTTTTTGCTACTTGTATGAGATATCACAGCGCAACCGT	1315
Qy	1201		CAGCTCCGCTCAGATGGTAAAAAGATGGTCATGTGCAGGATTTTACTGCTTTTGGGAT	1260
Db	1316		CAGCTCCGCTCAGATGGTAAAAAGATGGTCATGTGCAGGATTTTACTGCTTTTGGGAT	1375
Qy	1261		AAGGCATCAGAGACCCCAACTCTTCAAGGCTTTTCTTTTACTGTGTACAGCTGGCGAATTG	1320

Db 1376 AAGCATCAGAGACCCCAACTCTACAAAGCCCTTTCCTTTACTGTGACACCTGGCGAATTG 1435  
Qy 1321 TTAGCTGTGTCGCGCCCGTGGAGCAGGGAAGTCATCACTGTTPAAAGTGCCGTGCTCGG 1380  
Db 1436 TTAGCTGTGTCGCGCCCGTGGAGCAGGGAAGTCATCACTGTTPAAAGTGCCGTGCTCGG 1495  
Qy 1381 GAATTGCCCCAGTCAAGGCTGGTCAGCGTGCATGGAAGATTGCTATGTGTCAG 1440  
Db 1496 GAATTGCCCCAGTCAAGGCTGGTCAGCGTGCATGGAAGATTGCTATGTGTCAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAATAATTTATTTGGGAAAGAAATACGAA 1500  
Db 1556 CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAATAATTTATTTGGGAAAGAAATAGAA 1615  
Qy 1501 AAGGAACGATATGAAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1560  
Db 1616 AAGGAACGATATGAAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675  
Qy 1561 GAGGATGGTGCATCTGATGATAGGAGATCGGGGACCAAGCTGAGTGAGGGGCAGAAA 1620  
Db 1676 GAGGATGGTGCATCTGATAGGAGATCGGGGAAACCAAGCTGAGTGAGGGGCAGAAA 1735  
Qy 1621 GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT 1680  
Db 1736 GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT 1795  
Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACATTGTTGGAACCTGTGTATTTGTCAA 1740  
Db 1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACATTGTTGGAACCTGTGTATTTGTCAA 1855  
Qy 1741 ATTTTGCATGAGAGATCAAAATTTTGTAGTCACTCATCAGTTCAGTACCTCAAGCTGCA 1800  
Db 1856 ATTTTGCATGAGAGATCAAAATTTTGTAGTCACTCATCAGTTCAGTACCTCAAGCTGCA 1915  
Qy 1801 AGTCAGATTTCTGATATTGAAAGATGGTAAATGTGTGAGAGGGGACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTTCTGATATTGAAAGATGGTAAATGTGTGAGAGGGGACTTACACTGAGTTC 1975  
Qy 1861 CTAAAAATCTGGTATAGATTTTGGTCCCTTTTAAAGAAAGGATAATGAGGAAGTGAACAA 1920  
Db 1976 CTAAAAATCTGGTATAGATTTTGGTCCCTTTTAAAGAAAGGATAATGAGGAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGCGTTGG 1980  
Db 2036 CCTCCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGCGTTGG 2095  
Qy 1981 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2040  
Db 2096 TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2155  
Qy 2041 AATGTCAGGTACACTATACAGAGAGAACCGTTCGAAAGAAAGTTGGTTTTCAGGCC 2100  
Db 2156 AATGTCAGGTACACTATACAGAGAGAACCGTTCGAAAGAAAGTTGGTTTTCAGGCC 2215  
Qy 2101 TATAAGAAATTAATTCAGAGCTGGTGCACCTGGAATGTCCTATTTTCTTATTTCTCCTA 2160  
Db 2216 TATAAGAAATTAATTCAGAGCTGGTGCACCTGGAATGTCCTATTTTCTTATTTCTCCTA 2275  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTTCATCTCGGCAAC 2220  
Db 2276 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTGGTGGCTTTTCATCTCGGCAAC 2335  
Qy 2221 AACAAAGATATGCTAAATGTCACTGTAAATGGAGAGGAAATGTAAACGAGAACTAGAT 2280  
Db 2336 AACAAAGATATGCTAAATGTCACTGTAAATGGAGAGGAAATGTAAACGAGAACTAGAT 2395  
Qy 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTTTAACTGTAGCTACCGTTCTTTTGGCATA 2340  
Db 2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTTTAACTGTAGCTACCGTTCTTTTGGCATA 2455  
Qy 2341 GCAAGATCTCTATTTGGTATTTCTAGCTCCTGTTAACTCTTCAAAACTTTGCAACAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTTCTAGCTCCTGTTAACTCTTCAAAACTTTGCAACAA 2515

Qy 2401 ATGTTTGAATCAATTTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2460  
Db 2516 ATGTTTGAATCAATTTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCAAAAGACATTGGACACTTTGGATGATTTGTCGCGCTGACGCTTT 2520  
Db 2576 ATTTTAAATCGTTTCTCAAAAGACATTGGACACTTTGGATGATTTGTCGCGCTGACGCTTT 2635  
Qy 2521 TTAGATTTTCAATCAGACATTGCTCAAGTGGTTGGTGTGCTCTGTGGCTGTGCCCTG 2580  
Db 2636 TTAGATTTTCAATCAGACATTGCTCAAGTGGTTGGTGTGCTCTGTGGCTGTGCCCTG 2695  
Qy 2581 ATTCCTTGGATCGCAATACCCTTGGTTCCTTGGAAATCAATTTTCAATTTTCTTCGCGCA 2640  
Db 2696 ATTCCTTGGATCGCAATACCCTTGGTTCCTTGGAAATCAATTTTCAATTTTCTTCGCGCA 2755  
Qy 2641 TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGAAATCTACAACTCGGAGTCCAGTG 2700  
Db 2756 TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGAAATCTACAACTCGGAGTCCAGTG 2815  
Qy 2701 TTTTCCCACTTGTCACTTCTCTCAGGGGCTCTGGAACCATCCGGGCATACAAAGCAGAA 2760  
Db 2816 TTTTCCCACTTGTCACTTCTCTCAGGGGCTCTGGAACCATCCGGGCATACAAAGCAGAA 2875  
Qy 2761 GAGAGTGTCAAGNACTGTTTGTGACACACAGGATTTACATTCAGAGGCTTGGTTCTTG 2820  
Db 2876 GAGAGTGTCAAGNACTGTTTGTGACACACAGGATTTACATTCAGAGGCTTGGTTCTTG 2935  
Qy 2821 TTTTGGCAACGTCCTGCTGCTGCTGCTGATGCCATCTCTGATGCCATCTGTCATCTTGTGTC 2880  
Db 2936 TTTTGGCAACGTCCTGCTGCTGCTGCTGATGCCATCTCTGATGCCATCTGTCATCTTGTGTC 2995  
Qy 2881 ATCATCTGCTGCTTGGGTCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT 2940  
Db 2996 ATCATCTGCTGCTTGGGTCCTGATTTCTGGCAAAAACTCTGGATGCCGGCAGGTTGGT 3055  
Qy 2941 TTGGCACTGCTTATGCTGCTCAGCTCATCGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3000  
Db 3056 TTGGCACTGCTTATGCTGCTCAGCTCATCGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3115  
Qy 3001 GCTGAAGTTCAGAAATATGATGATCTCAGTAGAAAGGCTCATTTGAATACACAGACCTTGAA 3060  
Db 3116 GCTGAAGTTCAGAAATATGATGATCTCAGTAGAAAGGCTCATTTGAATACACAGACCTTGAA 3175  
Qy 3061 AAAGAACACCTTTGGGAATATCAGAAACGCCCAACACAGCCTGGCCCCATGAAAGAGTG 3120  
Db 3176 AAAGAACACCTTTGGGAATATCAGAAACGCCCAACACAGCCTGGCCCCATGAAAGAGTG 3235  
Qy 3121 ATATCTTTGACATGTGAATCTTCACTGACAGTCCAGTGGGCTCTGTTACTGCAAGCAT 3180  
Db 3236 ATATCTTTGACATGTGAATCTTCACTGACAGTCCAGTGGGCTCTGTTACTGCAAGCAT 3295  
Qy 3181 CTGACACACTCATTAAATCAAGAAAGGTTGGCAATTTGGGAAGAAACCGGAGCTGGA 3240  
Db 3296 CTGACACACTCATTAAATCAAGAAAGGTTGGCAATTTGGGAAGAAACCGGAGCTGGA 3355  
Qy 3241 AAAAGTTCCCTCATCTCAGGCCCTTTTAGATTGTFCAGAAACCGGAAGGTAAATTTGGATT 3300  
Db 3356 AAAAGTTCCCTCATCTCAGGCCCTTTTAGATTGTFCAGAAACCGGAAGGTAAATTTGGATT 3415  
Qy 3301 GATPAAGATCTTGACAACTGAAATTTGGAATTCAGATTTTAAAGGAAGAAATGTCATCAT 3360  
Db 3416 GATPAAGATCTTGACAACTGAAATTTGGAATTCAGATTTTAAAGGAAGAAATGTCATCAT 3475  
Qy 3361 CCTCAGGAACTCTGTTTGTTCATCTGGAACAAATGAGGAAAAACCTGGATCCCTTTAATGAG 3420  
Db 3476 CCTCAGGAACTCTGTTTGTTCATCTGGAACAAATGAGGAAAAACCTGGATCCCTTTAATGAG 3535  
Qy 3421 CACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCACTTGAA 3480  
Db 3536 CACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCACTTGAA 3595



Db 776 CAGCGATCGCAGTGAATCGCCCTACTCTGGATGAGATAGGAATATCGTGCCCTTGCTGGG 835  
Qy 721 ATGCGAGTCTAATCATCTCTGCGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA 780  
Db 836 ATGCGAGTCTAATCATCTCTGCGCCCTTGCAAGCTGTTTGGGAAGTTGTTCTCATCA 895  
Qy 781 CTGAGGAGTAAACCTGCAACTTTCCAGCATGCCAGATCAGGACCATGAATGAAGTTATA 840  
Db 896 CTGAGGAGTAAACCTGCAACTTTCCAGCATGCCAGATCAGGACCATGAATGAAGTTATA 955  
Qy 841 ACTGGTATAAGGATAATAAAATGTAGCCCTGGGAAAAGTCATTTCAAATCTTATTACC 900  
Db 956 ACTGGTATAAGGATAATAAAATGTAGCCCTGGGAAAAGTCATTTCAAATCTTATTACC 1015  
Qy 901 AATTGGAAGAAGAGAGATTTCAAGATTTCTGAGAAGTTCTCGCTCAGGGGGATGAAT 960  
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Qy 961 TTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCACCACTACGTG 1020  
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Qy 1021 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGAACGCTGTATGGGCT 1080  
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Db 1196 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGTGTGAGAGGGCAATC 1255  
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Db 1256 GTCAGCATCCGAAGAATCCAGACCTTTTGTGCTACTGTGATGAGATATCACAGCGCAACCGT 1315  
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Db 1316 CAGCTGCGCTCAGATGGTAAAGATGGTGCATGTCAGGATTTTACTGCTTTTTGGGAT 1375  
Qy 1261 AAGCATCAGAGACCCCACTCTACAGGCCCTTCTTCTTACTGTACAGACCTGGGCAATTG 1320  
Db 1376 AAGCATCAGAGACCCCACTCTACAGGCCCTTCTTCTTACTGTACAGACCTGGGCAATTG 1435  
Qy 1321 TTAGCTGTGTGGCGCGCTGGAGCAGGGAAGTCATCACTGTTAAGTGCCTGCTCGG 1380  
Db 1436 TTAGCTGTGTGGCGCGCTGGAGCAGGGAAGTCATCACTGTTAAGTGCCTGCTCGG 1495  
Qy 1381 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAAATGGCTATGTCTCAG 1440  
Db 1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAAATGGCTATGTCTCAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATAGAA 1500  
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Qy 1801 AGTCAGATTTCTGATATTGAAGATGGTAAATTGGTCAGAGGGGACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTTCTGATATTGAAGATGGTAAATTGGTCAGAGGGGACTTACACTGAGTTC 1975  
Qy 1861 CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATGAGGAAAGTGAACAA 1920  
Db 1976 CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATGAGGAAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAACCTCCACACATAAGAAATCGTACTCTCAGAGTCTTCCGGTTGG 1980  
Db 2036 CCTCCAGTTCAGGAACCTCCACACATAAGAAATCGTACTCTCAGAGTCTTCCGGTTGG 2095  
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Qy 2341 GCAAGATCTCTATTTGGTATTTCTAGCTCTTGTAACTCTTCAAAAATTTTGCACAAACAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTTCTAGCTCTTGTAACTCTTCAAAAATTTTGCACAAACAA 2515  
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Db 2756 TATTTTGGAAACGCTCAAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG 2815  
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Db 2876 GAGAGTGTTCAGGAACCTGTTTGGATGACACACAGGATTTTACATTCAGAGGCTTGGTTCTTG 2935  
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Db 2936 TTTTGGACAGCTCCCGCTGGTTCGCGCTCGTCTCGATGCCATCTGTGCCATGTGTTGTC 2995

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 Db CTGACAGCACTCATTAATCAAGAAAGGTGTGGCATTTGGGAAGAACCGGAGCTGGA 3355  
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 Db AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTGAGAACCCGAGGTAAATTTGGATT 3415  
 3301 GATAAGATCTTGACACTGAATTTGGACTTCAGATTTAAGGAAGAAATGTCATCATTA 3360  
 Db GATAAGATCTTGACACTGAATTTGGACTTCAGATTTAAGGAAGAAATGTCATCATTA 3475  
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 Db CCTCAGGAACCTGTTTGTTCACCTGGCAATAGGAAACCTGGATCCCTTTAAATGAG 3535  
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 Db CACACGATGAGGAACTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA 3595  
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 Db GATCTTCTGTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3655  
 3541 CAAGAACAACCTGCTGCTCCAGGCAATCTCAGGAAATATCAGATATGATGATGAT 3600  
 Db CAAGAACAACCTGCTGCTCCAGGCAATCTCAGGAAATATCAGATATGATGATGATGAT 3715  
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 3661 GAGAAATTTGCCACTGACCGCTGCTAACCTGACACAGATTTGAACACCATTAATTGAC 3720  
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 3721 AGCCACAAGATAATGTTTATGATTTAGATTTAGGAGAGATGGAAGATGATGATGATGAT 3780  
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 3841 GCGCTGCTGCTTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATATT 3900  
 Db GCGCTGCTGCTTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATATT 4015  
 3901 GGTACACTGACCATGCTGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 3960  
 Db GGTACACTGACCATGCTGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 4075  
 3961 TTCGAGACAGCACTGTGA 3978

4076 TTCGAGACAGCACTGTGA 4093  
 RESULT 8  
 AAH81778  
 ID AAH81778 standard; DNA; 4231 BP.  
 XX  
 AC AAH81778;  
 XX  
 DT 21-SEP-2001 (first entry)  
 XX  
 DE Human differential transcription-associated cDNA SEQ ID 287.  
 XX  
 KW Differential transcription; human; rat; tumour cell; cytostatic;  
 KW Ras modulator; Class II tumour suppressor gene; gene therapy; sa.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200157058-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 31-JAN-2001; 2001WO-EP001003.  
 XX  
 PR 31-JAN-2000; 2000DE-01004102.  
 XX  
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
 XX  
 PI Rosenthal A, Hinzmann B, Schaefer R, Zuber J, Tchernitsa O;  
 PI Grips M, Heilriegel M, Schmitz A, Sers C;  
 XX  
 DR WPI; 2001-483415/52.  
 XX  
 PT Nucleic acids differentially expressed between tumor and normal cells,  
 PT useful for diagnosis or therapy of tumors and for screening active  
 PT agents.  
 XX  
 PS Disclosure; Page 442-443; 579pp; German.  
 XX  
 CC This invention describes a nucleic acid (I) with differential expression  
 CC between tumor and normal cells and which has cytostatic activity. (I)  
 CC work as modulators of Ras activity by inducing expression of tumour  
 CC suppressor genes. (I), and polypeptides encoded by them, are useful as  
 CC targets for diagnosis or therapy and in screening to determine the  
 CC effects of an active compound (potential pharmaceutical) on a cell line,  
 CC particularly for diagnosis and treatment of tumors, especially by  
 CC modulating expression of (I) (by gene therapy, antisense RNA or ribozyme  
 CC methods) or by modulating the amount and/or location of (I)-encoded  
 CC polypeptides (by administration of the polypeptide or its activator,  
 CC antibody (optionally as a conjugate) or inhibitor). The method allows  
 CC identification of many Class II tumour suppressor genes (i.e. genes that  
 CC are not primary targets for tumour-initiating mutations). AAH81492-  
 CC AAH82376 represent the human and rat derived nucleic acid fragments  
 CC described in the method of the invention  
 XX  
 SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;  
 Query Match 99.9%; Score 3973.2; DB 5; Length 4231;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 ATGCTGCCCGTGTACCAAGGAGTGAAGCCCAACCCGCTGCAGGACGGAACCTCTGCTCA 60  
 Db 116 ATGCTGCCCGTGTACCAAGGAGTGAAGCCCAACCCGCTGCAGGACGGAACCTCTGCTCA 175  
 Qy 61 CGCGTGTCTTCTGCTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAGAG 120  
 Db 176 CGCGTGTCTTCTGCTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAGAG 235  
 Qy 121 GAAGATGATATGATTCAGTGTGCTGCCAGAGAACCGCTGCACAGCACCTTTGGAGAGAGTTG 180  
 Db 236 GAAGATGATATGATTCAGTGTGCTGCCAGAGAACCGCTGCACAGCACCTTTGGAGAGAGTTG 295

Qy 181 CAAGGGTCTGGGATAAAGAGTTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTA 240  
Db 296 CAAGGGTCTGGGATAAAGAGTTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTA 355  
Qy 241 ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTTGGGAAATTTTACGGTA 300  
Db 356 ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTTGGGAAATTTTACGGTA 415  
Qy 301 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAATTTTAAATATTTTT 360  
Db 416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAATTTTAAATATTTTT 475  
Qy 361 GAAATATATGATCCATGGATCTGTGGCTTTGAACACAGGGTACGCTATGCCACGGTG 420  
Db 476 GAAATATATGATCCATGGATCTGTGGCTTTGAACACAGGGTACGCTATGCCACGGTG 535  
Qy 421 CTGACTTTTTGACGCTCATTTTGGCTATCTGCACTCATATATTTTATFACGTTTCAG 480  
Db 536 CTGACTTTTTGACGCTCATTTTGGCTATCTGCACTCATATATTTTATFACGTTTCAG 595  
Qy 481 TGTCTCGGATGAGGTTACGAGTAGCCATGTCATATGATTTTATCGAAAGGCACTTCGT 540  
Db 596 TGTCTCGGATGAGGTTACGAGTAGCCATGTCATATGATTTTATCGAAAGGCACTTCGT 655  
Qy 541 CTTAGTAAATGCGCATGGGGAAGACAAACACAGCCAGATAGTCAATCTGCTGCCAAT 600  
Db 656 CTTAGTAAATGCGCATGGGGAAGACAAACACAGCCAGATAGTCAATCTGCTGCCAAT 715  
Qy 601 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTCTCTGTCGGCAGGACCACTG 660  
Db 716 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTCTCTGTCGGCAGGACCACTG 775  
Qy 661 CAGCGCATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATPATCGTCCTTGTGGG 720  
Db 776 CAGCGCATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATPATCGTCCTTGTGGG 835  
Qy 721 ATGCGAGTCTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTGTCTCATCA 780  
Db 836 ATGCGAGTCTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTGTCTCATCA 895  
Qy 781 CTGAGGAGTAAACTGCAACTTTTCAACGATGCCAGGATCAGGACCATGAATGAAGTTATA 840  
Db 896 CTGAGGAGTAAACTGCAACTTTTCAACGATGCCAGGATCAGGACCATGAATGAAGTTATA 955  
Qy 841 ACTGGTATAAGGATAATAAATAATGTAAGCTGGGAAAGTCATTTTCAAATCTTTATPAC 900  
Db 956 ACTGGTATAAGGATAATAAATAATGTAAGCTGGGAAAGTCATTTTCAAATCTTTATPAC 1015  
Qy 901 AATTTGAGAAAGAGGAGATTTCCAGATTTCTGAGAGTTCCCTGCCTCAGGGGATGAAT 960  
Db 1016 AATTTGAGAAAGAGGAGATTTCCAGATTTCTGAGAGTTCCCTGCCTCAGGGGATGAAT 1075  
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Db 1196 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGGTGTGAGAGGCAATC 1255  
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Qy 1261 AAGGCATCAGAGACCCCAACTCTACAGGCGCTTTCCTTTACTGTGCAGACCTGGCGAATTG 1320  
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Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
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Qy 1861 CTAAAACTCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATTAATGAGGAAAGTGAAACAA 1920  
Db 1976 CTAAAACTCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATTAATGAGGAAAGTGAAACAA 2035  
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Qy 2041 AATGTCCTCAGTTACACTATCAGAGGAAACCGTTTCTGAAAGAAAGTTGGTTTTCAGGCC 2100  
Db 2156 AATGTCCTCAGTTACACTATCAGAGGAAACCGTTTCTGAAAGAAAGTTGGTTTTCAGGCC 2215  
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Db 2216 TATAAGAAATTTACTTCAGAGCTGTGTCTCAGTGAATTTGTTCTTCAATTTTCTTCTCCTA 2275  
Qy 2161 AACACTCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTTATCTCTGGGCAAAAC 2220  
Db 2276 AACACTCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTTATCTCTGGGCAAAAC 2335  
Qy 2221 AAAACAAAGTATGCTTAAATGTCACTGTAAATGGAGGAGGAAATGTAAACGAGAACTAGAT 2280  
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QY 2581 ATTCCTTGGATCGCAATACCTTGGTTCCTCCCTGCGAATCATTTTCAATTTTCTTCGGCGA 2640  
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Db 2756 TATTTTGGAAAGCTCAAGAGATGTGAAGCGCCTGGAAATCTACAACCTCGGAGTCCAGTG 2815  
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Db 2816 TTTTCCCACTTGTCAATCTTCTCTCAGGGGCTCTGGACCACTCCGGGCATACAAGACGAA 2875  
QY 2761 GAGAGGTGTCAAGAACTGTGTGATGCAACACAGGATTTACATTCAGAGGCTTGGTCTTGT 2820  
Db 2876 GAGAGGTGTCAAGAACTGTGTGATGCAACACAGGATTTACATTCAGAGGCTTGGTCTTGT 2935  
QY 2821 TTTTGTGACAACTGTCGCGTGTGTCGCGTCTGGATGCCATCTGTGCCATGTTTGTCT 2880  
Db 2936 TTTTGTGACAACTGTCGCGTGTGTCGCGTCTGGATGCCATCTGTGCCATGTTTGTCT 2995  
QY 2881 ATCATCGTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGT 2940  
Db 2996 ATCATCGTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGT 3055  
QY 2941 TTGCACTGTCCTATGCCCTCACCTCATGCGGATGTTTTCAGTGGTGTGTTTCGCAAGT 3000  
Db 3056 TTGCACTGTCCTATGCCCTCACCTCATGCGGATGTTTTCAGTGGTGTGTTTCGCAAGT 3115  
QY 3001 GCTCAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3060  
Db 3116 GCTCAAGTTGAGATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAA 3175  
QY 3061 AAAGAAGCAGCTTGGGAATATCAGAAACGCCCAACACAGCCTGGCCCCATGAAGGAGTG 3120  
Db 3176 AAAGAAGCAGCTTGGGAATATCAGAAACGCCCAACACAGCCTGGCCCCATGAAGGAGTG 3235  
QY 3121 ATAATCTTTGACAACTGTGAACCTTCACTGACATCCAGTCCAGTGGGCTCTGGTACTGAAGCAT 3180  
Db 3236 ATAATCTTTGACAACTGTGAACCTTCACTGACATCCAGTCCAGTGGGCTCTGGTACTGAAGCAT 3295  
QY 3181 CTGACAGCACTCATTAATACAAGAAAGGTGTGCATTGTGGGAAGAACCGGAGCTGGA 3240  
Db 3296 CTGACAGCACTCATTAATACAAGAAAGGTGTGCATTGTGGGAAGAACCGGAGCTGGA 3355  
QY 3241 AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTTGTGAGAACCCGAGGTAAATTTGGATT 3300  
Db 3356 AAAAGTTCCCTCATCTCAGCCCTTTTATAGATTTGTGAGAACCCGAGGTAAATTTGGATT 3415  
QY 3301 GATAAGATCTTGACAACTGAATTTGGACTTCAGATTTAAGGAAGAAATGTCATCATTA 3360  
Db 3416 GATAAGATCTTGACAACTGAATTTGGACTTCAGATTTAAGGAAGAAATGTCATCATTA 3475  
QY 3361 CCTCAGGAACCTGTTTGTCTTCACTGGAACATGAGGAAAAACCTGGATCCCTTTAATAGAG 3420  
Db 3476 CCTCAGGAACCTGTTTGTCTTCACTGGAACATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535  
QY 3421 CACACGGATGAGGAACCTGTGGAATGCCCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3480

Db 3536 CACACGGATGAGGAACCTGTGGAATGCCCTTACAGAGGTACAACTTAAAGAAACCAATTGAA 3595  
QY 3481 GATCTTCTCTGTAATAATGGATACCTGAAATAGCAGAACTCAGGATCCAAATTTTAGTGTGGA 3540  
Db 3596 GATCTTCTCTGTAATAATGGATACCTGAAATAGCAGAACTCAGGATCCAAATTTTAGTGTGGA 3655  
QY 3541 CAAAGACAACTGGTGTGCTTGGCCAGGGCAATTTCTCAGGAAAAAATCAGATATTGATTATT 3600  
Db 3656 CAAAGACAACTGGTGTGCTTGGCCAGGGCAATTTCTCAGGAAAAAATCAGATATTGATTATT 3715  
QY 3601 GATCAAGGACGCAAAATGTGGATCCCAAGAACTGATGAGTTAAATACAAAAAATATCCGG 3660  
Db 3716 GATCAAGGACGCAAAATGTGGATCCCAAGAACTGATGAGTTAAATACAAAAAATATCCGG 3775  
QY 3661 GAGAAATTTGGCCCACTGACCGTGTCAACCAATTGACACAGATTTGAACCACTATTGAC 3720  
Db 3776 GAGAAATTTGGCCCACTGACCGTGTCAACCAATTGACACAGATTTGAACCACTATTGAC 3835  
QY 3721 AGCGACAAGATAAATGGTGTGATTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3780  
Db 3836 AGCGACAAGATAAATGGTGTGATTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3895  
QY 3781 TTGCTGCATAAATAAGAGAGCTTATTTTCAAGATGGTGCAACCACTGGGCAAGCAGAA 3840  
Db 3896 TTGCTGCATAAATAAGAGAGCTTATTTTCAAGATGGTGCAACCACTGGGCAAGCAGAA 3955  
QY 3841 GCCCTGCGCTCCTCAGTGAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATATT 3900  
Db 3956 GCCCTGCGCTCCTCAGTGAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATATT 4015  
QY 3901 GGTCACTGACACCATGGTTTACAAACACTTTCCAATGGACAGCCCTCGACCTTAACTATT 3960  
Db 4016 GGTCACTGACACCATGGTTTACAAACACTTTCCAATGGACAGCCCTCGACCTTAACTATT 4075  
QY 3961 TTCGAGACAGCACTGTGA 3978  
Db 4076 TTCGAGACAGCACTGTGA 4093

RESULT 9  
ADN39253  
ID ADN39253 standard; cDNA; 4231 BP.  
XX  
AC ADN39253;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:571.  
XX  
KW Human; differential expression; cancer; angiogenic disorder;  
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KW inflammatory disease; autoimmune disease;  
KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
KW detection; diagnosis; prognosis; drug screening; drug targeting;  
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
KW vulneryary; gene therapy; vaccine; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO2003042661-A2.  
XX  
PD 22-MAY-2003.  
XX  
PF 13-NOV-2002; 2002WO-US036810.  
XX  
PR 13-NOV-2001; 2001US-0350666P.  
PR 21-NOV-2001; 2001US-0332464P.  
PR 29-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335394P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-0355250P.



PR 13-FEB-2002; 2002US-0356714P.  
 PR 20-FEB-2002; 2002US-0359077P.  
 PR 29-MAR-2002; 2002US-0368809P.  
 PR 04-APR-2002; 2002US-0370110P.  
 PR 12-APR-2002; 2002US-0372246P.  
 PR 05-JUN-2002; 2002US-0386614P.  
 PR 16-JUL-2002; 2002US-0396839P.  
 PR 22-JUL-2002; 2002US-0397775P.  
 PR 22-JUL-2002; 2002US-0397845P.  
 PR 09-SEP-2002; 2002US-0409450P.  
 XX (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
 XX P-PSDB; ADN39254.  
 DR WPI; 2003-468649/44.  
 DR  
 XX Determining the presence or absence of a pathological cell in a patient,  
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
 PT a nucleic acid in a biological sample.  
 XX  
 PS Claim 8; SEQ ID NO 571; 1385pp; English.  
 XX  
 CC The invention relates to nucleic acids and proteins (ADN38693-ADN40064)  
 CC whose expression is upregulated or downregulated in specific cancers or  
 CC other diseases such as angioendothelial or fibrotic disorders, and to methods  
 CC of determining the presence or absence of a pathological cell in a  
 CC patient by detecting a nucleic acid at least 80% identical to those of  
 CC the invention or by detecting a polypeptide of the invention. The  
 CC invention also relates to expression vectors and host cells comprising a  
 CC nucleic acid of the invention; antibodies which specifically bind a  
 CC polypeptide of the invention; use of such antibodies for drug targeting;  
 CC and methods of screening for modulators of activity or expression of the  
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
 CC antibodies and methods are useful for diagnosing, prognosing and treating  
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
 CC neovascularization syndromes, scarring and uterine fibroids. They may  
 CC also be useful in wound healing and in contraception. The present  
 CC sequence represents a nucleic acid sequence of the invention.  
 XX  
 SX Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;  
 SX

Query Match 99.9%; Score 3973.2; DB 11; Length 4231;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCTGCCGTGTACAGAGGTGAAGCCCAACCGCTGCGAGGACGGAACTCTGCTCA 60  
 DB |||||  
 QY 116 ATGCTGCCGTGTACAGAGGTGAAGCCCAACCGCTGCGAGGACGGAACTCTGCTCA 175  
 DB |||||  
 QY 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTAAATTTGGCCATAAAGGAGATTAGAG 120  
 DB |||||  
 QY 176 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTAAATTTGGCCATAAAGGAGATTAGAG 235  
 DB |||||  
 QY 121 GAAGATGATATGATATTCAGTCTGCGAAGAACCGCTCACAGCACCTTTGGAGAGATTG 180  
 DB |||||  
 QY 236 GAAGATGATATGATATTCAGTCTGCGAAGAACCGCTCACAGCACCTTTGGAGAGATTG 295  
 DB |||||  
 QY 181 CAAGGTTCTGGATAAGAGATTTTAAGAGCTGAGATGAGACGACAGAGCCCTTCTTTA 240  
 DB |||||  
 QY 296 CAAGGTTCTGGATAAGAGATTTTAAGAGCTGAGATGAGACGACAGAGCCCTTCTTTA 355  
 DB |||||  
 QY 241 ACAAGAGCAATCATAAAGTGTACTTGGAAATCTTATTTAGTTTGGGAAATTTTACGTGA 300  
 DB |||||  
 QY 356 ACAAGAGCAATCATAAAGTGTACTTGGAAATCTTATTTAGTTTGGGAAATTTTACGTGA 415  
 DB |||||  
 QY 301 ATTGAGGAAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAATTTATTTATTTT 360  
 DB |||||  
 QY 416 ATTGAGGAAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAATTTATTTATTTT 475  
 DB |||||

QY 361 GAAAAATTATGATCCCATGGATTCTGTGGCTTTGAAACAGCGTACGCTATGCCACGGTG 420  
 DB |||||  
 QY 476 GAAAAATTATGATCCCATGGATTCTGTGGCTTTGAAACAGCGTACGCTATGCCACGGTG 535  
 DB |||||  
 QY 421 CTGACTTTTTGACAGCGTCATTTTGGCTATATCTGCATCACTTATATTTTATCAGTTCAAG 480  
 DB |||||  
 QY 536 CTGACTTTTTGACAGCGTCATTTTGGCTATATCTGCATCACTTATATTTTATCAGTTCAAG 595  
 DB |||||  
 QY 481 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAGGCACTTCGT 540  
 DB |||||  
 QY 596 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGGAGGCACTTCGT 655  
 DB |||||  
 QY 541 CTTAGTAAATGCGCATGCGGAGAGCAACACAGCGCAGATAGTCAATCTCTCTGTCCAAT 600  
 DB |||||  
 QY 656 CTTAGTAAATGCGCATGCGGAGAGCAACACAGCGCAGATAGTCAATCTCTCTGTCCAAT 715  
 DB |||||  
 QY 601 GATGTGAACAAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGTGGGACAGCACTG 660  
 DB |||||  
 QY 716 GATGTGAACAAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTCTGTGGGACAGCACTG 775  
 DB |||||  
 QY 661 CAGCGCATGCGAGTACTGCGCTACTCTGATGAGATAGGAATATCGTGCCTTCTGCTGG 720  
 DB |||||  
 QY 776 CAGCGCATGCGAGTACTGCGCTACTCTGATGAGATAGGAATATCGTGCCTTCTGCTGG 835  
 DB |||||  
 QY 721 ATGCGAGTCTTAATCAATCTCTGCGCTTGCAGAACTGTTTGGGAAAGTGTCTCTCATCA 780  
 DB |||||  
 QY 836 ATGCGAGTCTTAATCAATCTCTGCGCTTGCAGAACTGTTTGGGAAAGTGTCTCTCATCA 895  
 DB |||||  
 QY 781 CTGAGGAGTAAAACTGCAACTTTTACCGATGCCAGATCAGGACCATGAATGAAGTTATA 840  
 DB |||||  
 QY 896 CTGAGGAGTAAAACTGCAACTTTTACCGATGCCAGATCAGGACCATGAATGAAGTTATA 955  
 DB |||||  
 QY 841 ACTGATATAGGATAATAAANAATGATAGCTGCGGAAAAGTCNTTTTCAATCTTATTACC 900  
 DB |||||  
 QY 956 ACTGATATAGGATAATAAANAATGATAGCTGCGGAAAAGTCNTTTTCAATCTTATTACC 1015  
 DB |||||  
 QY 901 AATTGGAAGAAGAGAGATTCTCAAGATTCTGAGAAAGTTCCTCCCTCAGGGGATGAAT 960  
 DB |||||  
 QY 1016 AATTGGAAGAAGAGAGATTCTCAAGATTCTGAGAAAGTTCCTCCCTCAGGGGATGAAT 1075  
 DB |||||  
 QY 961 TTGCTTTCTGTTTTTCTAGTGAAGCAAAATCATCGTGTGTGTGACCTTCAACCCTACGGT 1020  
 DB |||||  
 QY 1076 TTGCTTTCTGTTTTTCTAGTGAAGCAAAATCATCGTGTGTGTGACCTTCAACCCTACGGT 1135  
 DB |||||  
 QY 1021 CTCTCGGAGTGTGATCAGCGAGCCGCGTGTTCGTGCGAGTGAAGCTGTATGGGGCT 1080  
 DB |||||  
 QY 1136 CTCTCGGAGTGTGATCAGCGAGCCGCGTGTTCGTGCGAGTGAAGCTGTATGGGGCT 1195  
 DB |||||  
 QY 1081 GTGCGGCTGACGGTTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1140  
 DB |||||  
 QY 1196 GTGCGGCTGACGGTTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1255  
 DB |||||  
 QY 1141 GTCAGCATCCGAAGAAATCCAGACCTTTTGTACTTGTATGAGATATCACAGCGCAACCGT 1200  
 DB |||||  
 QY 1256 GTCAGCATCCGAAGAAATCCAGACCTTTTGTACTTGTATGAGATATCACAGCGCAACCGT 1315  
 DB |||||  
 QY 1201 CAGTCCGCTCAGATGTGTAAGAAAGATGTCATGTCAGGATTTTACTGCTTTTGGAT 1260  
 DB |||||  
 QY 1316 CAGTCCGCTCAGATGTGTAAGAAAGATGTCATGTCAGGATTTTACTGCTTTTGGAT 1375  
 DB |||||  
 QY 1261 AAGCATCAGAGACCCCAACTCTCAAGGCTTTCTTTACTGTGAGACCTGGGGAATG 1320  
 DB |||||  
 QY 1376 AAGCATCAGAGACCCCAACTCTCAAGGCTTTCTTTACTGTGAGACCTGGGGAATG 1435  
 DB |||||  
 QY 1321 TTAGTCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCACTGTTTAAAGTCCGCTGCTCGG 1380  
 DB |||||  
 QY 1436 TTAGTCTGTGTCGCGCCCGTGGGAGCAGGGAAGTCACTGTTTAAAGTCCGCTGCTCGG 1495  
 DB |||||  
 QY 1381 GAATGGCCCCAAGTCAAGGCTGTCAGCGTGCATGGAAGAAATGCTATGCTCTCAG 1440  
 DB |||||  
 QY 1496 GAATGGCCCCAAGTCAAGGCTGTCAGCGTGCATGGAAGAAATGCTATGCTCTCAG 1555  
 DB |||||  
 QY 1441 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGAA 1500  
 DB |||||



Qy 3661 GAGAAATTCGCCACTGCACGCTGCTAACCAATTCACACACAGATTGACACCATTTATTGAC 3720  
 Db 3776 GAGAAATTCGCCACTGCACGCTGCTAACCAATTCACACACAGATTGACACCATTTATTGAC 3835  
 Qy 3721 AGCGACAGATAATGGTGTATGATTCAGGAACTGAAAGATATGATGAGCCGTATGTT 3780  
 Db 3836 AGCGACAGATAATGGTGTATGATTCAGGAACTGAAAGATATGATGAGCCGTATGTT 3895  
 Qy 3781 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGTTGCAACAACTGGGCAAGGCAGAA 3840  
 Db 3896 TTGCTGCAAAATAAGAGAGCCTATTTTACAAGATGTTGCAACAACTGGGCAAGGCAGAA 3955  
 Qy 3841 GCCCTGCCCTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATTT 3900  
 Db 3956 GCCCTGCCCTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTATCCACATTT 4015  
 Qy 3901 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACATTT 3960  
 Db 4016 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACATTT 4075  
 Qy 3961 TTCGAGACAGCACTGTGA 3978  
 Db 4076 TTCGAGACAGCACTGTGA 4093

RESULT 10  
 ADR66822  
 ID ADR66822 standard; DNA; 5832 BP.  
 XX  
 AC ADR66822;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Human prostatic carcinoma derived DNA SEQ ID 115 #4.  
 XX  
 KW human; cytostatic; diagnosis; prostatic cancer;  
 KW differential expression analysis; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004076614-A2.  
 XX  
 PD 10-SEP-2004.  
 XX  
 XX 22-FEB-2004; 2004WO-DE000433.  
 XX  
 XX 27-FEB-2003; 2003DE-01009985.  
 PR 14-MAY-2003; 2003DE-01022134.  
 XX  
 XX (HINZ/) HINZMANN B.  
 PA (DAHL/) DAHL E.  
 PA (ROSE/) ROSENTHAL A.  
 PA (HERM/) HERMANN K.  
 PA (PILA/) PILARSKY C.  
 XX  
 PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
 PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
 PI Xinzhang L, Staub B;  
 XX  
 XX WPI; 2004-653386/63.  
 XX  
 XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
 PT useful for diagnosis, treatment and in screening for specific binding  
 PT agents.  
 PT  
 XX  
 PS Claim 1; Page 1348-1349; 1607pp; German.  
 XX  
 CC This invention describes novel cytostatic polynucleotide and polypeptide  
 CC sequences which can be used in a method for diagnosing prostatic cancer  
 CC or the risk of developing prostatic cancer. Diagnosis is based on  
 CC determining over transcription or over expression of the sequences in  
 CC prostatic tissue. Screening for inhibitors of the sequences or detection

CC substances involves a binding assay, any compounds that bind are  
 CC selected, optionally after deconvolution of mixtures. Detection of a  
 CC predetermined minimum level of the reporter indicates the presence of  
 CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
 CC short-interfering RNA or ribozymes; an organic molecule of molecular  
 CC weight below 5000, preferably 300, that binds to the polypeptide; an  
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
 CC (monoclonal) antibody directed against Ab or any of the above derivatised  
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
 CC radioisotope. The polynucleotides are identified in human prostatic  
 CC cancer by differential expression analysis, using DNA microarrays,  
 CC between normal and tumorous tissues, with (over)expression being detected  
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
 CC prostatic cancer patients, or subjects at risk, were incubated  
 CC sequentially with anti-human CD4 murine monoclonal antibodies;  
 CC biotinylated second antibody; streptavidin-conjugated horseradish  
 CC peroxidase and then diaminobenzidine as colour former (brown). The  
 CC samples were counterstained with hemalum (blue). Malignant cells stained  
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
 CC lymph node metastases were also stained. ADR65805-ADR6594 represent the  
 CC polynucleotide and polypeptide sequences used in the method of the  
 CC invention.

XX  
 SQ Sequence 5832 BP; 1660 A; 1175 C; 1306 G; 1691 T; 0 U; 0 Other;  
 Query Match 99.9%; Score 3973.2; DB 13; Length 5832;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 ATGCTGCCCGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAATCTGTCTCA 60  
 Db 116 ATGCTGCCCGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAATCTGTCTCA 175  
 Qy 61 CGCGTGTCTTCGTGGCTCAATCCCTCTGTTTAAATTTGCCATAACCGAGATTAGAG 120  
 Db 176 CGCGTGTCTTCGTGGCTCAATCCCTCTGTTTAAATTTGCCATAACCGAGATTAGAG 235  
 Qy 121 GAAGATGATATGATTTTCAAGTGTCTGCCAAGAGACCGCTCACAGCACCTTGGAGAGGTTG 180  
 Db 236 GAAGATGATATGATTTTCAAGTGTCTGCCAAGAGACCGCTCACAGCACCTTGGAGAGGTTG 295  
 Qy 181 CAAGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGAGATGAGAGAGCCCTTCTTTA 240  
 Db 296 CAAGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGAGATGAGAGAGCCCTTCTTTA 355  
 Qy 241 ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAATTTTACGTTA 300  
 Db 356 ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAATTTTACGTTA 415  
 Qy 301 ATTGAGGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTT 360  
 Db 416 ATTGAGGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTT 475  
 Qy 361 GAAATTTATGATCCCATGATTTCTGTGGCTTTGAAACAGAGGTACGCTATGCCACGGTG 420  
 Db 476 GAAATTTATGATCCCATGATTTCTGTGGCTTTGAAACAGAGGTACGCTATGCCACGGTG 535  
 Qy 421 CTGACTTTTTCGACGCTCATTTTGGCTTATCTGCTCACTTATATTTTATCACGTTTCAG 480  
 Db 536 CTGACTTTTTCGACGCTCATTTTGGCTTATCTGCTCACTTATATTTTATCACGTTTCAG 595  
 Qy 481 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTTTCGGAAGGCACTTCGT 540  
 Db 596 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTTTCGGAAGGCACTTCGT 655  
 Qy 541 CTTAGTAACATGGCCATGGGAGAGACAAACACAGCCAGATAGTCAATCTGCTGTCNAAT 600  
 Db 656 CTTAGTAACATGGCCATGGGAGAGACAAACACAGCCAGATAGTCAATCTGCTGTCNAAT 715  
 Qy 601 GATGTGAACAAGTTTGATCATAGGTGACAGTGTCTTACACTTCTCTGTGGGAGGACCACTG 660

Db 716 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGCAGGACCACTG 775  
Qy 661 CAGCGCATCGCAGTACTGCCCTACTCTGAGTGAGATAGGAATATCGTCTTGCTGGG 720  
Db 776 CAGCGCATCGCAGTACTGCCCTACTCTGAGTGAGATAGGAATATCGTCTTGCTGGG 835  
Qy 721 ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTTGTTCTCATCA 780  
Db 836 ATGCGAGTCTTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTTGTTCTCATCA 895  
Qy 781 CTGAGGAGTAAACTGCAACTTTTCACCGATGCCAGGATCAGGACCATGAATGAATTATA 840  
Db 896 CTGAGGAGTAAACTGCAACTTTTCACCGATGCCAGGATCAGGACCATGAATGAATTATA 955  
Qy 841 ACTGGTATAAGGATAATAAAAAATGTACGCCCTGGGAAAAGTCATTTTCAAATCTTATTACC 900  
Db 956 ACTGGTATAAGGATAATAAAAAATGTACGCCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015  
Qy 901 AATTGGAAGAAGAGAGATTTTCAAGATTCTGAGAAAGTTCTGSCCTCAGGGGGATGAAT 960  
Db 1016 AATTGGAAGAAGAGAGATTTTCAAGATTCTGAGAAAGTTCTGSCCTCAGGGGGATGAAT 1075  
Qy 961 TTGGCTTCGTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTTCACCACTACGTG 1020  
Db 1076 TTGGCTTCGTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTTCACCACTACGTG 1135  
Qy 1021 CTCCTCGCAGTGTGATCACAGCCAGCCGCGTGTCTGTCAGTGCAGCTGTATGGGGCT 1080  
Db 1136 CTCCTCGCAGTGTGATCACAGCCAGCCGCGTGTCTGTCAGTGCAGCTGTATGGGGCT 1195  
Qy 1081 GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGTCAGAGGCAATC 1140  
Db 1196 GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGTCAGAGGCAATC 1255  
Qy 1141 GTGAGCATCCGAGAAATCCAGACTTTTGTGCTACTTGTATGAGATATCACAGCGCAACCGT 1200  
Db 1256 GTGAGCATCCGAGAAATCCAGACTTTTGTGCTACTTGTATGAGATATCACAGCGCAACCGT 1315  
Qy 1201 CAGTCGCCGTGAGATGTAAAGATGTCATGTCAGTGCAGGATTTTACTGCTTTTGGGAT 1260  
Db 1316 CAGTCGCCGTGAGATGTAAAGATGTCATGTCAGTGCAGGATTTTACTGCTTTTGGGAT 1375  
Qy 1261 AAGGCATCAGAGACCCCACTCTACAAGGCTTTCTTTACTGTGACACCTGCGCAATTG 1320  
Db 1376 AAGGCATCAGAGACCCCACTCTACAAGGCTTTCTTTACTGTGTCAGACCTGGCGAATTG 1435  
Qy 1321 TTAGCTGTGTCGCGCCCGTGGGAGCAGGAAAGTCACTGTTTAAAGTGCCTGCTCGG 1380  
Db 1436 TTAGCTGTGTCGCGCCCGTGGGAGCAGGAAAGTCACTGTTTAAAGTGCCTGCTCGG 1495  
Qy 1381 GAATTGSCCCCAAGTCAAGGCTGTCAGCGTGCATCGAAGAAATGCTATGTCTCAG 1440  
Db 1496 GAATTGSCCCCAAGTCAAGGCTGTCAGCGTGCATCGAAGAAATGCTATGTCTCAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
Db 1556 CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615  
Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1560  
Db 1616 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675  
Qy 1561 GAGGATGTCATCTGACTGTGATAGGATCGGGGAACCACTGAGTGGAGGCGAGAAA 1620  
Db 1676 GAGGATGTCATCTGACTGTGATAGGATCGGGGAACCACTGAGTGGAGGCGAGAAA 1735  
Qy 1621 GCAGGGTAAACCTTGAAGAGAGTCTATCAAGATGTCGACATCTATCTCTCGAGCAT 1680  
Db 1736 GCAGGGTAAACCTTGAAGAGAGTCTATCAAGATGTCGACATCTATCTCTCGAGCAT 1795  
Qy 1681 CCTCTCAGTGCAGTATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTATTTGTCAA 1740

Db 1796 CCTCTCAGTGCAGTATGATCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTTGTCAA 1855  
Qy 1741 ATTTTGATCAGAGAAGATCAAAATTTTAGTGACTCATCAGTTGCACTACCTCAAAAGCTGCA 1800  
Db 1856 ATTTTGATCAGAGAAGATCAAAATTTTAGTGACTCATCAGTTGCACTACCTCAAAAGCTGCA 1915  
Qy 1801 AGTCAGATTCGTATATTTGAAAGATGTTAAATGTTGTCAGAAAGGGACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTCGTATATTTGAAAGATGTTAAATGTTGTCAGAAAGGGACTTACACTGAGTTC 1975  
Qy 1861 CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAGGATATATGAGGAAAGTGAACAA 1920  
Db 1976 CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAGGATATATGAGGAAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCCGTTTGG 1980  
Db 2036 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCCGTTTGG 2095  
Qy 1981 TCTCAACAATCTTCTAGACCTCTTGAAGATGTTGCTCTGAGAGCCGAAGATACAGAG 2040  
Db 2096 TCTCAACAATCTTCTAGACCTCTTGAAGATGTTGCTCTGAGAGCCGAAGATACAGAG 2155  
Qy 2041 AATGTCCCAGTTACACTATCAGAGGAAACCGTCTGAAAGGAAGTGGTTTTCAGGCC 2100  
Db 2156 AATGTCCCAGTTACACTATCAGAGGAAACCGTCTGAAAGGAAGTGGTTTTCAGGCC 2215  
Qy 2101 TATAAGAAATTTACTTACAGAGTGGTCTCACTGATGTTCTTCAATTTCTTATTTCTCTTA 2160  
Db 2216 TATAAGAAATTTACTTACAGAGTGGTCTCACTGATGTTCTTCAATTTCTTATTTCTCTTA 2275  
Qy 2161 AACACTGCACTCAGTTGCTATGTTCTCAAGATTTGGTGGCTTTTCACTGCGCAAAAC 2220  
Db 2276 AACACTGCACTCAGTTGCTATGTTCTCAAGATTTGGTGGCTTTTCACTGCGCAAAAC 2335  
Qy 2221 AACAAAGTATGTAATGTCACCTGTAATGAGGAGGAATGTAACCGAGAACTAGAT 2280  
Db 2336 AACAAAGTATGTAATGTCACCTGTAATGAGGAGGAATGTAACCGAGAACTAGAT 2395  
Qy 2281 CTTAACTGGTACTTAAAGATTTTAACTCAGGTTTAACTGTAGTACCGTCTCTTTTGGGATA 2340  
Db 2396 CTTAACTGGTACTTAAAGATTTTAACTCAGGTTTAACTGTAGTACCGTCTCTTTTGGGATA 2455  
Qy 2341 GCAAGATCTCTATTTGTTTCTACGTCCTTTGTTTAACTTTTCAAAAATTTTGCACAAACAA 2400  
Db 2456 GCAAGATCTCTATTTGTTTCTACGTCCTTTGTTTAACTTTTCAAAAATTTTGCACAAACAA 2515  
Qy 2401 ATGTTTGAATCAATCTGAAAGCTCCGGTATTTATTTTGTATAGAAATCCAATAGGAAGA 2460  
Db 2516 ATGTTTGAATCAATCTGAAAGCTCCGGTATTTATTTTGTATAGAAATCCAATAGGAAGA 2575  
Qy 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGTCGCGCTGACGTTT 2520  
Db 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGTCGCGCTGACGTTT 2635  
Qy 2521 TTAGATTTTCAATCAGACATTTGCTACAGTGGTGGTGGTGTCTCTGTGGCTGTGGCGGTG 2580  
Db 2636 TTAGATTTTCAATCAGACATTTGCTACAGTGGTGGTGGTGTCTCTGTGGCTGTGGCGGTG 2695  
Qy 2581 ATTCTTGGATCCGAATACCTTTGGTTCCCTTTGGGAATCAATTTTCAATTTTCTTCGCGGA 2640  
Db 2696 ATTCTTGGATCCGAATACCTTTGGTTCCCTTTGGGAATCAATTTTCAATTTTCTTCGCGGA 2755  
Qy 2641 TATTTTGGAAACGTCAAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG 2700  
Db 2756 TATTTTGGAAACGTCAAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG 2815  
Qy 2701 TTTTCCCACTTGTCTCTCTCCAGGGGCTCTGGACCACTCCGGGCATACAAAGCAGAA 2760  
Db 2816 TTTTCCCACTTGTCTCTCTCCAGGGGCTCTGGACCACTCCGGGCATACAAAGCAGAA 2875  
Qy 2761 GAGAGTGTGAGAACTGTTTGTATGACACACAGATTTTACATTCAGAGGCTTGTGTTCTTG 2820  
Db 2876 GAGAGTGTGAGAACTGTTTGTATGACACACAGATTTTACATTCAGAGGCTTGTGTTCTTG 2935

Qy 2821 TTTTGTGACAAAGCTCCCGCTGGTTCGCGTCCGTCTGGATGCCATCTCTGTCATGTTTGTGTC 2880  
Db 2936 TTTTGTGACAAAGCTCCCGCTGGTTCGCGTCCGTCTGGATGCCATCTCTGTCATGTTTGTGTC 2995  
Qy 2881 ATCATCGTTGCTTGTGGTCCCTGATTTCTGGCAAAAACCTCTGGATGCGCGCAGGTTGGT 2940  
Db 2996 ATCATCGTTGCTTGTGGTCCCTGATTTCTGGCAAAAACCTCTGGATGCGCGCAGGTTGGT 3055  
Qy 2941 TTGGCATGCTCTATGCGCTCACGCTCATGGGGATGTTTTCAGTGGTGTGTTCGACAAAAT 3000  
Db 3056 TTGGCATGCTCTATGCGCTCACGCTCATGGGGATGTTTTCAGTGGTGTGTTCGACAAAAT 3115  
Qy 3001 GCTGAAGTGTGAGATATGATGATCTCTAGTAGAAGGCTCATTTGATATACACAGACCTTGAA 3060  
Db 3116 GCTGAAGTGTGAGATATGATGATCTCTAGTAGAAGGCTCATTTGATATACACAGACCTTGAA 3175  
Qy 3061 AAGAAGCAGCTTGGGAATATCAGAAACGCCACACAGCCTGGCCCCCATGAAGAGTG 3120  
Db 3176 AAGAAGCAGCTTGGGAATATCAGAAACGCCACACAGCCTGGCCCCCATGAAGAGTG 3235  
Qy 3121 ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3180  
Db 3236 ATAATCTTTGACAAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3295  
Qy 3181 CTGACAGCACTTAATATCACAGAAAAGGTTGGCAATTTGGGAAAGAACCGGAGCTGGA 3240  
Db 3296 CTGACAGCACTTAATATCACAGAAAAGGTTGGCAATTTGGGAAAGAACCGGAGCTGGA 3355  
Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTTCAGAACCCGAAAGGTAAATTTGGATT 3300  
Db 3356 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTTCAGAACCCGAAAGGTAAATTTGGATT 3415  
Qy 3301 GATAAGATCTTGACAACTGAAATTTGSACTTCAAGATTTAAGGAAGAAAATGTCAATCAT 3360  
Db 3416 GATAAGATCTTGACAACTGAAATTTGSACTTCAAGATTTAAGGAAGAAAATGTCAATCAT 3475  
Qy 3361 CCTCAGGACCTGTTTGTTCACCTGGACATGAGGAAAACCTGGATCCCTTTAATGAG 3420  
Db 3476 CCTCAGGACCTGTTTGTTCACCTGGACATGAGGAAAACCTGGATCCCTTTAATGAG 3535  
Qy 3421 CACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA 3480  
Db 3536 CACACGATGAGGAACCTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA 3595  
Qy 3481 GATCTTCTGTGTAATGATCTGAAATTAGCAGAACTCAGATCCAATTTTATGTTGGGA 3540  
Db 3596 GATCTTCTGTGTAATGATCTGAAATTAGCAGAACTCAGATCCAATTTTATGTTGGGA 3655  
Qy 3541 CAAAGCAACTGTTGCTTGCCTGCGGCAATTTCTCAGGAAATTCAGATATTCATTTATT 3600  
Db 3656 CAAAGCAACTGTTGCTTGCCTGCGGCAATTTCTCAGGAAATTCAGATATTCATTTATT 3715  
Qy 3601 GATGAAGCGACGCAAAATGTGGATCCAGAACTGATGATTTAATACAAAAAATCCGG 3660  
Db 3716 GATGAAGCGACGCAAAATGTGGATCCAGAACTGATGATTTAATACAAAAAATCCGG 3775  
Qy 3661 GAGAAATTTGCCCATGCTGACCGTGTCAACCATTCAGACAGATTTGAACCATTTATTGAC 3720  
Db 3776 GAGAAATTTGCCCATGCTGACCGTGTCAACCATTCAGACAGATTTGAACCATTTATTGAC 3835  
Qy 3721 AGCAGCAAGATTAATGTTTGTAGATTTCAGGAGACTGGAAGATATGATGACCCGTATGTT 3780  
Db 3836 AGCAGCAAGATTAATGTTTGTAGATTTCAGGAGACTGGAAGATATGATGACCCGTATGTT 3895  
Qy 3781 TTGCTGCAAAATAAAGAGAGCTATTTTACAAAGTGTGCAACAACTGGGCAAGCGAGAA 3840  
Db 3896 TTGCTGCAAAATAAAGAGAGCTATTTTACAAAGTGTGCAACAACTGGGCAAGCGAGAA 3955  
Qy 3841 GCCGCTGCTCATCTGAAACAGCAAAACAGGATATCTTCAAAAGAAATTTATCCACATATT 3900  
Db 3956 GCCGCTGCTCATCTGAAACAGCAAAACAGGATATCTTCAAAAGAAATTTATCCACATATT 4015

Qy 3901 GGTCACACTGACACATGGTTTCAAAACACTTCCAAATGGACAGCCTCGACCTTAACTATT 3960  
Db 4016 GGTCACACTGACACATGGTTTCAAAACACTTCCAAATGGACAGCCTCGACCTTAACTATT 4075  
Qy 3961 TTCGAGACAGCACTGTGA 3978  
Db 4076 TTCGAGACAGCACTGTGA 4093  
RESULT 11  
ADRE5919  
ID ADR65919 standard; DNA; 5832 BP.  
XX ADR65919;  
XX AC ADR65919;  
XX DT 02-DEC-2004 (first entry)  
XX DE Human prostatic carcinoma derived DNA SEQ ID 115 #1.  
XX KW human; cytostatic; diagnosis; prostatic cancer;  
XX KW differential expression analysis; ds.  
XX OS Homo sapiens.  
XX PN WO2004076614-A2.  
XX PD 10-SEP-2004.  
XX PF 22-FEB-2004; 2004WO-DE000433.  
XX PR 27-FEB-2003; 2003DE-01009985.  
XX PR 14-MAY-2003; 2003DE-01022134.  
XX PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
PI Xinzhong L, Staub E;  
XX WPI; 2004-653386/63.  
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.  
XX Claim 1; Page 177-178; 1607pp; German.  
XX This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are  
CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;

CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminebenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.

SQ Sequence 5832 BP; 1660 A; 1175 C; 1306 G; 1691 T; 0 U; 0 Other;

Query Match 99.9%; Score 3973.2; DB 13; Length 5832;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGCTGCCGCTGATACGAGGAGTGAAGCCCAACCGCTGCAGGACGCGAACTCTGCTCA	60
Db	116	ATGCTGCCGCTGATACGAGGAGTGAAGCCCAACCGCTGCAGGACGCGAACTCTGCTCA	175
Qy	61	CGCGTGTCTCTCGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAGAG	120
Db	176	CGCGTGTCTCTCGTGGCTCAATCCCTTGTTTAAATTTGGCCATAAACGGAGATTAGAG	235
Qy	121	GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG	180
Db	236	GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTTGGAGAGAGTTG	295
Qy	181	CAAGGGTTCGGGATAAAGAAGTTTAAAGACTGAGAATGAGCCACAGAACGCTTCTTTA	240
Db	296	CAAGGGTTCGGGATAAAGAAGTTTAAAGACTGAGAATGAGCCACAGAACGCTTCTTTA	355
Qy	241	ACAAGAGCAATCATAAAGTGTTACTTGGAAATCTTATTTAGTTTTCGGAAATTTTACGTTA	300
Db	356	ACAAGAGCAATCATAAAGTGTTACTTGGAAATCTTATTTAGTTTTCGGAAATTTTACGTTA	415
Qy	301	ATTGAGAAAGTGCNAAAGTAATCCAGCCCATATTTTTGGAAAAATTTAATTAATTTTT	360
Db	416	ATTGAGAAAGTGCNAAAGTAATCCAGCCCATATTTTTGGAAAAATTTAATTAATTTTT	475
Qy	361	GAANAATTATGATCCCATGGATTCTGTGGCTTTGAAACACAGCGTAGCCCTATGCCACGGTG	420
Db	476	GAANAATTATGATCCCATGGATTCTGTGGCTTTGAAACACAGCGTAGCCCTATGCCACGGTG	535
Qy	421	CTGACTTTTTTGCAGCGCTCATTTTGGCTATACTGCAATCACTTATATTTTTTATCACGTTCCAG	480
Db	536	CTGACTTTTTTGCAGCGCTCATTTTGGCTATACTGCAATCACTTATATTTTTTATCACGTTCCAG	595
Qy	481	TGTGCTCGGATAGAGTTACGAGTAGCCATGTGCCATATGATTTATTCGGAAGGCACCTCGT	540
Db	596	TGTGCTCGGATAGAGTTACGAGTAGCCATGTGCCATATGATTTATTCGGAAGGCACCTCGT	655
Qy	541	CTTAGTAAACATGGCCATGGGGAAGACAACACAGGCCAGATAGTCATCTGCTGTCCAAAT	600
Db	656	CTTAGTAAACATGGCCATGGGGAAGACAACACAGGCCAGATAGTCATCTGCTGTCCAAAT	715
Qy	601	GATGTGAACAAGTTTGTATCAGGTGACAGTGTTCTTACACTTCTCTGTGGGAGGACCACTG	660
Db	716	GATGTGAACAAGTTTGTATCAGGTGACAGTGTTCTTACACTTCTCTGTGGGAGGACCACTG	775
Qy	661	CAGCGCATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTGCGG	720
Db	776	CAGCGCATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGTGCGG	835
Qy	721	ATGGCAGTTCTTAATCATTTCTCTGCCCTTGCNAAAGCTGTTTTGGGAAGTTGTTCTCATCA	780
Db	836	ATGGCAGTTCTTAATCATTTCTCTGCCCTTGCNAAAGCTGTTTTGGGAAGTTGTTCTCATCA	895
Qy	781	CTGAGGAGTAAACTGCAACTTTTCACCGATGCGAGGATCAGGACCATCAATGAAGTTATA	840
Db	896	CTGAGGAGTAAACTGCAACTTTTCACCGATGCGAGGATCAGGACCATGAAGTTATA	955
Qy	841	ACTGGTATAAGGATAAATAAAATGTACGCCCTGGGAAAAAGTCATTTTCAAATCTTTATTACC	900







DE Prostate cancer marker cDNA.  
 KW Prostate; cancer; cytostatic; gene therapy; marker; ss.  
 XX Homo sapiens.  
 OS WO2003009814-A2.  
 XX PD 06-FEB-2003.  
 XX PF 25-JUL-2002; 2002WO-US023913.  
 XX PR 25-JUL-2001; 2001US-0307982P.  
 PR 22-AUG-2001; 2001US-0314356P.  
 PR 25-SEP-2001; 2001US-0325020P.  
 PR 12-DEC-2001; 2001US-0341746P.  
 PR 05-MAR-2002; 2002US-0362158P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX PA Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;  
 XX PI Hoersht S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;  
 XX DR WPI; 2003-248033/24.  
 DR P-PSDB; ADB75178.  
 XX New nucleic acid molecule, useful for diagnosing or treating prostate  
 PT cancer.  
 XX Claim 1; SEQ ID NO 1; 99pp; English.  
 XX The invention relates to newly discovered cancer markers associated with  
 CC the cancerous state of prostate cells. Also disclosed is a method of  
 CC assessing whether a patient is afflicted with prostate cancer. The method  
 CC of the invention involves assessing whether a patient is afflicted with  
 CC prostate cancer by comparing the level of expression of a marker in a  
 CC patient sample and the normal level of expression of the marker in a  
 CC control non-prostate cancer sample, where a significant increase in the  
 CC level of expression of the marker in the patient sample and the normal  
 CC level indicates that the patient is afflicted with prostate cancer.  
 CC Nucleic acids of the invention are useful for diagnosing or treating  
 CC prostate cancer, and may be useful in gene therapy. Sequences given in  
 CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 5870 BP; 1698 A; 1174 C; 1306 G; 1692 T; 0 U; 0 Other;

Query Match 99.9%; Score 3973.2; DB 10; Length 5870;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 301 ATTGAGGAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTT 360  
 Db 416 ATTGAGGAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTT 475  
 Qy 361 GAAAAATTATGATCCCATGGAATTCCTGGCTTTTGAACACAGCGTAGCCCTATGCCACGGTG 420  
 Db 476 GAAAAATTATGATCCCATGGAATTCCTGGCTTTTGAACACAGCGTAGCCCTATGCCACGGTG 535  
 Qy 421 CTGACTTTTGGCAGCGTCATTTTGGCTATCTGTCATCACTTATATTTTATCAGTTTCAG 480  
 Db 536 CTGACTTTTGGCAGCGTCATTTTGGCTATCTGTCATCACTTATATTTTATCAGTTTCAG 595  
 Qy 481 TGTGCTGGGATAGGTTTACGAGTAGCCATATGTCATATGATTTATCGGAAGCACTTCGT 540  
 Db 596 TGTGCTGGGATAGGTTTACGAGTAGCCATATGTCATATGATTTATCGGAAGCACTTCGT 655  
 Qy 541 CTTAGTAACATGGCCATGGGGAAGACAAACACAGCCGAGATAGTCAATCTGCTGTCCAAT 600  
 Db 656 CTTAGTAACATGGCCATGGGGAAGACAAACACAGCCGAGATAGTCAATCTGCTGTCCAAT 715  
 Qy 601 GATGTGAACAAAGTTTGAATCAGGTGACAGTGTCTTACACTTCTGTTGGGAGGACCACTG 660  
 Db 716 GATGTGAACAAAGTTTGAATCAGGTGACAGTGTCTTACACTTCTGTTGGGAGGACCACTG 775  
 Qy 661 CAGCGCATCGCAGTGAATGCGCTACTCTGGATGAGATAGGAATATCTGTCCTTGTCTGG 720  
 Db 776 CAGCGCATCGCAGTGAATGCGCTACTCTGGATGAGATAGGAATATCTGTCCTTGTCTGG 835  
 Qy 721 ATGCGATGTTAATCATCTCTGCTTCTGCAAGCTGTTTGGGAAGTGTCTTCTCATCA 780  
 Db 836 ATGCGATGTTAATCATCTCTGCTTCTGCAAGCTGTTTGGGAAGTGTCTTCTCATCA 895  
 Qy 781 CTGAGGAGTAAACTGCAACTTTTACCGATGCCAGGATCAGGACCATCAATGAAGTTATA 840  
 Db 896 CTGAGGAGTAAACTGCAACTTTTACCGATGCCAGGATCAGGACCATCAATGAAGTTATA 955  
 Qy 841 ACTGTTAAGGATTAATAAATAATGACCGCTGGGAAAGTCAATTTTCAAACTTTATTTACC 900  
 Db 956 ACTGTTAAGGATTAATAAATAATGACCGCTGGGAAAGTCAATTTTCAAACTTTATTTACC 1015  
 Qy 901 AATTGAGAAGAGGAGATTTCAAGATTTCTGAGAAGTTCTGCTCAGGGGAGATGAAT 960  
 Db 1016 AATTGAGAAGAGGAGATTTCAAGATTTCTGAGAAGTTCTGCTCAGGGGAGATGAAT 1075  
 Qy 961 TTGCTTCTGTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCAACCACTACGCTG 1020  
 Db 1076 TTGCTTCTGTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCAACCACTACGCTG 1135  
 Qy 1021 CTCCTCGCAGTGTGATCACAGCCAGCGCGGTGTTCTGTCAGTGAAGCTGTATGGGGCT 1080  
 Db 1136 CTCCTCGCAGTGTGATCACAGCCAGCGCGGTGTTCTGTCAGTGAAGCTGTATGGGGCT 1195  
 Qy 1081 GTGCGGTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGGTGTTCAGAGGCAATC 1140  
 Db 1196 GTGCGGTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGGTGTTCAGAGGCAATC 1255  
 Qy 1141 GTGAGCATCGAAGATCCAGACCTTTTGTCTACTTGTGATGAGATATCACAGCGCAACCGT 1200  
 Db 1256 GTGAGCATCGAAGATCCAGACCTTTTGTCTACTTGTGAGATATCACAGCGCAACCGT 1315  
 Qy 1201 CAGCTGCGGTGAGATGTTAAAGATGTTGTCAGTGTGAGGATTTTACTGCTTTTGGGAT 1260  
 Db 1316 CAGCTGCGGTGAGATGTTAAAGATGTTGTCAGTGTGAGGATTTTACTGCTTTTGGGAT 1375  
 Qy 1261 AAGGCATCAGAGACCCCACTCTCAAGGCTTTTCTTTACTGTCAAGCTGTGGCAATG 1320  
 Db 1376 AAGGCATCAGAGACCCCACTCTCAAGGCTTTTCTTTACTGTCAAGCTGTGGCAATG 1435  
 Qy 1321 TTAGCTGTGTCGGCCCCCGTGGGAGCAGGAAGTCACTATGTTAAAGTCCGCTCTCGG 1380  
 Db 1436 TTAGCTGTGTCGGCCCCCGTGGGAGCAGGAAGTCACTATGTTAAAGTCCGCTCTCGG 1495  
 Qy 1381 GAATTGSCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGATTTGCTGTCTCAG 1440

Db	1496	GAATGGCCCAAGTCACGGGCTGGTCAGCGTGATGGAGAAATTCCTATGTGTCACAG	1555
Qy	1441	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAATATTTATTTGGGAAGAAATACGAA	1500
Db	1556	CAGCCCTGGGTGTTCTCGGGAACCTCTGAGGAGTAATATTTATTTGGGAAGAAATATGAA	1615
Qy	1501	AAGGAACGATATGAAAAAGTCATAAAGCTTGTCCTCTGAAAAAGGATTTACAGCTGTTG	1560
Db	1616	AAGGAACGATATGAAAAAGTCATAAAGCTTGTCCTCTGAAAAAGGATTTACAGCTGTTG	1675
Qy	1561	GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGAGGGGACAGAA	1620
Db	1676	GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGAGGGGACAGAA	1735
Qy	1621	GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT	1680
Db	1736	GCACGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGACGAT	1795
Qy	1681	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1740
Db	1796	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA	1855
Qy	1741	ATTTTGCATGAGAGATCACAAATTTTAGTGACTCATCAGTTGTCAGTACCTCAAAGCTGCA	1800
Db	1856	ATTTTGCATGAGAGATCACAAATTTTAGTGACTCATCAGTTGTCAGTACCTCAAAGCTGCA	1915
Qy	1801	AGTCAGATTTCTGATATTTGAAAGATGGTAAATAGTGCAGAGGGGACTTACACTGAGTTC	1860
Db	1916	AGTCAGATTTCTGATATTTGMAAGATGGTAAATAGTGCAGAGGGGACTTACACTGAGTTC	1975
Qy	1861	CTAAAACTCGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA	1920
Db	1976	CTAAAACTCGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA	2035
Qy	1921	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG	1980
Db	2036	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG	2095
Qy	1981	TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCCAAGATACAGAG	2040
Db	2096	TCTCAACAAATCTTCTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCCAAGATACAGAG	2155
Qy	2041	AATGTCACGTTACACTATCAGAGAGAACCGTTCTGAGGAAAGTTGGTTTTCAGGCC	2100
Db	2156	AATGTCACGTTACACTATCAGAGAGAACCGTTCTGAGGAAAGTTGGTTTTCAGGCC	2215
Qy	2101	TATAAGAAATTAATTCAGAGCTGGTGCTCAGTGGATTTGTTCTATTTCTTATTTCTCTTA	2160
Db	2216	TATAAGAAATTAATTCAGAGCTGGTGCTCAGTGGATTTGTTCTATTTCTTATTTCTCTTA	2275
Qy	2161	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGCTTTTATCTGGGCAAC	2220
Db	2276	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGCTTTTATCTGGGCAAC	2335
Qy	2221	AAACAAAGTATGCTAAATGTCACGTAAATGGAGGAGGAATGTAAACGAGAACTAGAT	2280
Db	2336	AAACAAAGTATGCTAAATGTCACGTAAATGGAGGAGGAATGTAAACGAGAACTAGAT	2395
Qy	2281	CTTAACTGGTACTTAGGAAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGGATA	2340
Db	2396	CTTAACTGGTACTTAGGAAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGGATA	2455
Qy	2341	GCAAGATCTCTATTTGGTATTTCTAGCTCCTTGTAACTCTTCAACAACTTTGCAACAAA	2400
Db	2456	GCAAGATCTCTATTTGGTATTTCTAGCTCCTTGTAACTCTTCAACAACTTTGCAACAAA	2515
Qy	2401	ATGTTTGAGTCAATTCGAAAGCTCCGGTATTTATTTGATAGAAATCCAAATAGGAAGA	2460
Db	2516	ATGTTTGAGTCAATTCGAAAGCTCCGGTATTTATTTGATAGAAATCCAAATAGGAAGA	2575
Qy	2461	ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTTGTGCGCGCTGACGTTT	2520

Db	2576	ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACGTTT	2635
Qy	2521	TTAGATTTTCATCCAGACATTTGCTACAAGTGGTTGGTGTGCTCTCTGTGGCTGTGGCCGTG	2580
Db	2636	TTAGATTTTCATCCAGACATTTGCTACAAGTGGTTGGTGTGCTCTGTGGCTGTGGCCGTG	2695
Qy	2581	ATTCCTTTGGATCGCAATACCTTTGGTTCCCTCTGGAAATCATTTTTCATTTTCTTCGGCGA	2640
Db	2696	ATTCCTTTGGATCGCAATACCTTTGGTTCCCTCTGGAAATCATTTTTCATTTTCTTCGGCGA	2755
Qy	2641	TATTTTGGAAAACTCAAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG	2700
Db	2756	TATTTTGGAAAACTCAAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG	2815
Qy	2701	TTTTTCCACTTTGTTCATCTTCTCCAGGGGCTTGGAACCATCCGGGCATATAAAGACGAA	2760
Db	2816	TTTTTCCACTTTGTTCATCTTCTCCAGGGGCTTGGAACCATCCGGGCATATAAAGACGAA	2875
Qy	2761	GAGAGGTGTCAGGAACCTGTTTGATGACACACAGGATTTACATTCAGAGGCTTGGTTCCTG	2820
Db	2876	GAGAGGTGTCAGGAACCTGTTTGATGACACACAGGATTTACATTCAGAGGCTTGGTTCCTG	2935
Qy	2821	TTTTTGAACACGTCGCCGCTGCTCGCGTCTGGATGCCATCTGTGCCATGTGTTGTC	2880
Db	2936	TTTTTGAACACGTCGCCGCTGCTCGCGTCTGGATGCCATCTGTGCCATGTGTTGTC	2995
Qy	2881	ATCATCTGTTGGCTTGGGTCCTGATTTCTGGCAAAAACTCTGGATCGGGCAGGTTGGT	2940
Db	2996	ATCATCTGTTGGCTTGGGTCCTGATTTCTGGCAAAAACTCTGGATCGGGCAGGTTGGT	3055
Qy	2941	TTGSCACTGCTCTATGCCCCACGCTCATGSGGATGTTTCAGTGGTGTGTTTCGACAAAGT	3000
Db	3056	TTGSCACTGCTCTATGCCCCACGCTCATGSGGATGTTTCAGTGGTGTGTTTCGACAAAGT	3115
Qy	3001	GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATGTAATACACAGACTTGAA	3060
Db	3116	GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATGTAATACACAGACTTGAA	3175
Qy	3061	AAAGAACACCTTTGGGAATATCAGAAACGCCACACACAGGCTGGCCCCATGAAGGATG	3120
Db	3176	AAAGAACACCTTTGGGAATATCAGAAACGCCACACACAGGCTGGCCCCATGAAGGATG	3235
Qy	3121	ATAATCTTTGACAAATGTGAACCTTCATGTCACAGTCCAGTGGGCTCTGTTGTAAGCAT	3180
Db	3236	ATAATCTTTGACAAATGTGAACCTTCATGTCACAGTCCAGTGGGCTCTGTTGTAAGCAT	3295
Qy	3181	CTGACAGCACTCAATTAATCAAGAAAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA	3240
Db	3296	CTGACAGCACTCAATTAATCAAGAAAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA	3355
Qy	3241	AAAAGTTCCCTCATCTCAGCCCTTTTATGATTGTTCAGAACCCGGAAGTTAAAATTTGGATT	3300
Db	3356	AAAAGTTCCCTCATCTCAGCCCTTTTATGATTGTTCAGAACCCGGAAGTTAAAATTTGGATT	3415
Qy	3301	GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTTAAGGAAGAAAAATGCTCAATCAT	3360
Db	3416	GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTTAAGGAAGAAAAATGCTCAATCAT	3475
Qy	3361	CCTCAGGAACCTGTTTTTGTTCACCTGGAAACATAGAGAAAAACCTGGATCCCTTTAATGAG	3420
Db	3476	CCTCAGGAACCTGTTTTTGTTCACCTGGAAACATAGAGAAAAACCTGGATCCCTTTAATGAG	3535
Qy	3421	CACACGATGAGGAACCTGTGGATGCTTACAGAGGTACAACTTAAGAAACCACTTGAA	3480
Db	3536	CACACGATGAGGAACCTGTGGATGCTTACAGAGGTACAACTTAAGAAACCACTTGAA	3595
Qy	3481	GATCTTCTGTAAAAATGGATGAAATAGCAGAAATCAGGATCCAAATTTTAGTGTTCGA	3540
Db	3596	GATCTTCTGTAAAAATGGATGAAATAGCAGAAATCAGGATCCAAATTTTAGTGTTCGA	3655
Qy	3541	CAAAAGCAACTGGTGTGCTTGGCAGGGCAATTCACAGGAAAAATCAGATATGATTAAT	3600
Db	3656	CAAAAGCAACTGGTGTGCTTGGCAGGGCAATTCACAGGAAAAATCAGATATGATTAAT	3715



Db 716 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGTGGGAGGACCACCTG 775  
Qy 661 CAGCGGATCGCAGTGAATGCGCTTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 720  
Db 776 CAGCGGATCGCAGTGAATGCGCTTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835  
Qy 721 ATGCGAGTCTTAATCATTTCTCTGCTCCCTTGCAAGCTGTTTGGGAAGTGTCTCATCA 780  
Db 836 ATGCGAGTCTTAATCATTTCTGCTCCCTTGCAAGCTGTTTGGGAAGTGTCTCATCA 895  
Qy 781 CTGAGGAGTAAACTGCAACTTTTCAAGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 840  
Db 896 CTGAGGAGTAAACTGCAACTTTTCAAGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 955  
Qy 841 ACTGGTATAGGATTAATAAATGTAAGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 900  
Db 956 ACTGGTATAGGATTAATAAATGTAAGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 1015  
Qy 901 AATTTGAGAAAGAGGAGATTTTCAAGATTTCTGAGAAAGTTCTGCTCCCTCAGGGGATGAAT 960  
Db 1016 AATTTGAGAAAGAGGAGATTTTCAAGATTTCTGAGAAAGTTCTGCTCCCTCAGGGGATGAAT 1075  
Qy 961 TTGCTTTCGTTTTTTCAGTGAAGCAAAATCATCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020  
Db 1076 TTGCTTTCGTTTTTTCAGTGAAGCAAAATCATCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1135  
Qy 1021 CTCTCGCGAGTGTGATCAGCGCAGCGCGGTGTCTGCGCAGTGAAGCTGTATGGGGCT 1080  
Db 1136 CTCTCGCGAGTGTGATCAGCGCAGCGCGGTGTCTGCGCAGTGAAGCTGTATGGGGCT 1195  
Qy 1081 GTGGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGTTGTGAGAGGCAATC 1140  
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Qy 1141 GTCAGCATCCGAAGAATCCAGACCTTTTGTACTTGTGATGAGATATCAGCGCAACCGT 1200  
Db 1256 GTCAGCATCCGAAGAATCCAGACCTTTTGTACTTGTGATGAGATATCAGCGCAACCGT 1315  
Qy 1201 CAGCTGCGCTCAGATGTGTAAGATGCTGATGTGAGGATTTTACTGCTTTTGGGAT 1260  
Db 1316 CAGCTGCGCTCAGATGTGTAAGATGCTGATGTGAGGATTTTACTGCTTTTGGGAT 1375  
Qy 1261 AAGGCATCAGAGACCCCACTCTAAGAGCCTTTCTTTTACTGTGAGACCTGGCGAATTG 1320  
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Db 1436 TTAGCTGTGTGCGCCCGTGGGAGCAGGGAAGTCACTGTTTAAAGTGGCGTCTCGGG 1495  
Qy 1381 GAATTGGCCCAAGTCAAGGCTGCTGAGTGTGATGAGGATTTGCTATGTGCTCAG 1440  
Db 1496 GAATTGGCCCAAGTCAAGGCTGCTGAGTGTGATGAGGATTTGCTATGTGCTCAG 1555  
Qy 1441 CAGCCCTGGGTGTTCTCGGGAATCTCAGGAGTAAATTTTATTTGGGAAGAAATACGAA 1500  
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Qy 1561 GAGGATGCTGATCTGATGATAGGAGATCGGGGAACCGCTGAGTGGAGGCGAGAA 1620  
Db 1676 GAGGATGCTGATCTGATGATAGGAGATCGGGGAACCGCTGAGTGGAGGCGAGAA 1735  
Qy 1621 GCAGGCTGAACCTTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGAGAT 1680  
Db 1736 GCAGGCTGAACCTTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGAGAT 1795  
Qy 1681 CCTCTCAGTGCAGTATGCGGAAGTTAGCAGACACTTTGTTGCAACTGTGTATTGTCAA 1740  
Db 1796 CCTCTCAGTGCAGTATGCGGAAGTTAGCAGACACTTTGTTGCAACTGTGTATTGTCAA 1855

Qy 1741 ATTTTGATCAGAGATCAAAATTTTAGTGACTCATCAGTTGCAGTACCTCAAGCTGCA 1800  
Db 1856 ATTTTGATCAGAGATCAAAATTTTAGTGACTCATCAGTTGCAGTACCTCAAGCTGCA 1915  
Qy 1801 AGTCAGATTTCTGATATTGAAAGATGTAAGATGCTGAGAGGAGCTTACACAGTTC 1860  
Db 1916 AGTCAGATTTCTGATATTGAAAGATGTAAGATGCTGAGAGGAGCTTACACAGTTC 1975  
Qy 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAA 1920  
Db 1976 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAA 2035  
Qy 1921 CCTCCAGTTCAGGAATCTCCACACTAAGGAATCGTACTTCTCAGAGTCTTTCGGTTTG 1980  
Db 2036 CCTCCAGTTCAGGAATCTCCACACTAAGGAATCGTACTTCTCAGAGTCTTTCGGTTTG 2095  
Qy 1981 TCTCAACAATCTTCTAGACCTCTCTTGAAGATGGTCTCTCGGAGAGCCCAAGATACAGAG 2040  
Db 2096 TCTCAACAATCTTCTAGACCTCTCTTGAAGATGGTCTCTCGGAGAGCCCAAGATACAGAG 2155  
Qy 2041 AATGTCCAGTTTACATATCAGAGGAAACCGTTCTGAAGAAAGTTGGTTTTTCAGGCC 2100  
Db 2156 AATGTCCAGTTTACATATCAGAGGAAACCGTTCTGAAGAAAGTTGGTTTTTCAGGCC 2215  
Qy 2101 TATAAGAAATTTACTTTTACAGAGTGGTCTCACTGGAATCTTCTATTTTCTTTTCTCTTA 2160  
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Qy 2341 GCAAGATCTCTATTGGTATTCTAGCTCTTTTAACTCTTCAAAAATTTTGCACAACAA 2400  
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Qy 2401 ATGTTTGAGTCAATTTGAAAGCTCCGGTATTATCTTTGATAGAAATCCAAATAGGAGA 2460  
Db 2516 ATGTTTGAGTCAATTTGAAAGCTCCGGTATTATCTTTGATAGAAATCCAAATAGGAGA 2575  
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Qy 2521 TTAGATTTTCAATCCAGACATTTGCTAACAGTGGTGGTGTGTGTGTGTGTGTGTGTGTGT 2580  
Db 2636 TTAGATTTTCAATCCAGACATTTGCTAACAGTGGTGGTGTGTGTGTGTGTGTGTGTGTGT 2695  
Qy 2581 ATTCCTTGGATCGCAATACCTTTGGTTCCCTTTGGAAATCATTTTTCATTTTCTTCGGCA 2640  
Db 2696 ATTCCTTGGATCGCAATACCTTTGGTTCCCTTTGGAAATCATTTTTCATTTTCTTCGGCA 2755  
Qy 2641 TATTTTGGAAACGTCACAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG 2700  
Db 2756 TATTTTGGAAACGTCACAGAGATGTGAAGCGCTGGAATCTCAAACTCGGAGTCCAGTG 2815  
Qy 2701 TTTTCCCACTTGTCTATCTTCTCCAGGGCTCTGGACCAATCCGGGCAATACAAAGAGAA 2760  
Db 2816 TTTTCCCACTTGTCTATCTTCTCCAGGGCTCTGGACCAATCCGGGCAATACAAAGAGAA 2875  
Qy 2761 GAGAGGTGTGAGGAACTGTTTGTATGACACAGAGATTTTACATTCAGAGGCTTGTCTTGT 2820  
Db 2876 GAGAGGTGTGAGGAACTGTTTGTATGACACAGAGATTTTACATTCAGAGGCTTGTCTTGT 2935

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QY 3001 GCTGAAGTTGAGAAATGATGATCTCAGTAGAAGAGGTCATTTGAATACACAGACCTTGAA 3060
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Db 3536 CACACGATGAGGAACTGTGGATGCTTACAGAGGTACAACTTAAGAAACCATTTGAA 3595
QY 3481 GATCTTCTCGTAAATAGGATCTGAATTAGCAATCAGATCCAAATTTTAGTGTGGA 3540
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QY 3661 GAGAAATTTCCCACTGACCGTGTAAACCATTTGACACAGATTTGAACCATTTATTGAC 3720
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QY 3721 AGCGCAAGATATGTTTTAGATTACGGAAGACTGAAAGATATGATAGCCGTATGTT 3780
Db 3836 AGCGCAAGATATGTTTTAGATTACGGAAGACTGAAAGATATGATAGCCGTATGTT 3895
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QY 3841 GCCGCTGCCCTCACTGAAACAGCAAAACAGTATCTTTCAAAAGAAATTTACACATATT 3900
Db 3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGTATCTTTCAAAAGAAATTTACACATATT 4015
QY 3901 GGTCACTGACACATGTTGTTACAAACACATTTCCAATGGACAGCCCTCGACCTTAACTATT 3960
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Db 4016 GGTCACTGACCATGCTGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACATT 4075
QY 3961 TTCGAGACAGCACTGTGA 3978
Db 4076 TTCGAGACAGCACTGTGA 4093

RESULT 14
AAH93828
ID AAH93828 standard; cDNA; 6082 BP.
XX
AC AAH93828;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific 1st full length cDNA sequence for P510S.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN W0200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001574.
XX
PR 14-JAN-2000; 2000US-00483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Mesgher WJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
PS Claim 1; Page 411-412; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used to treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAH01115 to AAH01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 6082 BP; 1721 A; 1249 C; 1357 G; 1755 T; 0 U; 0 Other;
Query Match 99.7%; Score 3966; DB 4; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ATGCTGCCCTGTGATACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCAACCTCTGTGTC 60
Db 186 ATGCTGCCCTGTGATACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCAACCTCTGTGTC 245
QY 61 CGCGTGTCTTCTTGTGGTGGCTCAATCCCTTGTAAATTCGCCATAAACCGAGATTAGAG 120
Db 246 CGCGTGTCTTCTTGTGGTGGCTCAATCCCTTGTAAATTCGCCATAAACCGAGATTAGAG 305
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QY 121 GAAGATGATATGTTTCAAGTCTGCCAGAGACCGCTCAGCACCTTGGAGGAGTTG 180  
DB 306 GAAGATGATATGTTTCAAGTCTGCCAGAGACCGCTCAGCACCTTGGAGGAGTTG 365  
QY 181 CAAGGGTCTCGGATAAAGAAAGTTTAAAGAGTGAAGATACGACACAGAGCCCTTCTTTA 240  
DB 366 CAAGGGTCTCGGATAAAGAAAGTTTAAAGAGTGAAGATACGACACAGAGCCCTTCTTTA 425  
QY 241 ACAAGACAATCAPAAGTGTACTGGAATCTTATTTTAAAGTGTGGAATTTTACGTTA 300  
DB 426 ACAAGACAATCAPAAGTGTACTGGAATCTTATTTTAAAGTGTGGAATTTTACGTTA 485  
QY 301 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAAATTAATATTTT 360  
DB 486 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAAATTAATATTTT 545  
QY 361 GAAATTTATCATCCATCGGATTCGTGGCTTTGAAACACAGCGTACGCTATGCCACGGTG 420  
DB 546 GAAATTTATGATCCATCGGATTCGTGGCTTTGAAACACAGCGTACGCTATGCCACGGTG 605  
QY 421 CTGACTTTTTCACGCTCATTTTGGCTTATCTGCAATCACTTATATTTTATFACGTTTCA 480  
DB 606 CTGACTTTTTCACGCTCATTTTGGCTTATCTGCAATCACTTATATTTTATFACGTTTCA 665  
QY 481 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCATCTCGT 540  
DB 666 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCATCTCGT 725  
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DB 1026 ACTGGTATAGGATAATAAAGATGACGCTGGGAAAAGTCAATTTTCAATCTTATTTACC 1085  
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DB 1326 GTCAGCAATCCAGAAATCCAGACCTTTTGTGCTATTTGATGAGATATCAGCGCAACCGT 1385

QY 1201 CAGCTCCGTCAGATGGTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT 1260  
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QY 1801 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGGTGCAGAAAGGGAATTAACCTGAGTTTC 1860  
DB 1986 AGTCAGATTTCTGATATTTGAAAGATGGTAAATGGTGCAGAAAGGGAATTAACCTGAGTTTC 2045  
QY 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA 1920  
DB 2046 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA 2105  
QY 1921 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCCGTTTGG 1980  
DB 2106 CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCCGTTTGG 2165  
QY 1981 TCTCAACAAATCTTCTAGACCTCTTGAAGATGGTGTCTCTGGAGAGCCAGATACAGAG 2040  
DB 2166 TCTCAACAAATCTTCTAGACCTCTTGAAGATGGTGTCTCTGGAGAGCCAGATACAGAG 2225  
QY 2041 AATGTCAGGTATACACTATCAGAGGAAACCGTTCTGAAGAAAGTGGTTTTCAGGCC 2100  
DB 2226 AATGTCAGGTATACACTATCAGAGGAAACCGTTCTGAAGAAAGTGGTTTTCAGGCC 2285  
QY 2101 TATAAGAAATTTACTTTCAGAGCTGGTGTCTCAGTGAATGTCTTCTATTTTCTTATCTCCTA 2160  
DB 2286 TATAAGAAATTTACTTTCAGAGCTGGTGTCTCAGTGAATGTCTTCTATTTTCTTATCTCCTA 2345  
QY 2161 AACACTCGAGTCAAGTTGCTGTATGCTTCAAGATTTGGTGGCTTTTCTATCTGGGCAAC 2220  
DB 2346 AACACTCGAGTCAAGTTGCTGTATGCTTCAAGATTTGGTGGCTTTTCTATCTGGGCAAC 2405  
QY 2221 AACAAAGTATGCTAAATGTCACTGAATGGAGGAGGAATGTAAACGAGAGCTAGAT 2280  
DB 2406 AACAAAGTATGCTAAATGTCACTGAATGGAGGAGGAATGTAAACGAGAGCTAGAT 2465  
QY 2281 CTTAACTGGTACTTATAGGAATTTTATTCAGGTTTAACTGTAGCTACCGTCTTTTGGGCATA 2340



Db 2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2525  
Qy 2341 GCAAGATCTCTATTGGTATTCTACGTCCTTGTGTAATCTTACAACTTTGACAAACAA 2400  
Db 2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTGTAATCTTACAACTTTGACAAACAA 2585  
Qy 2401 ATGTTTGAGTCAATCTCAAGCTCCGGTATATTCTTTGTAGAGAAATCCAATAGGAAGA 2460  
Db 2586 ATGTTTGAGTCAATCTCAAGCTCCGGTATATTCTTTGTAGAGAAATCCAATAGGAAGA 2645  
Qy 2461 ATTTTAAATCGTTTCTCAAGACATTTGACACTTTGGATGATTGCTGCCGCTGACGTTT 2520  
Db 2646 ATTTTAAATCGTTTCTCAAGACATTTGACACTTTGGATGATTGCTGCCGCTGACGTTT 2705  
Qy 2521 TTAGATTTTCACTCAGACATTCGCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2580  
Db 2706 TTAGATTTTCACTCAGACATTCGCTCAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2765  
Qy 2591 ATTCTTGGATCGCAATACCTTGGTTCCTTGGTTCCTTGGATTCATTTTCATTTTCTTGGCGA 2640  
Db 2766 ATTCTTGGATCGCAATACCTTGGTTCCTTGGTTCCTTGGATTCATTTTCATTTTCTTGGCGA 2825  
Qy 2641 TATTTTGGAAACGTCAGAGATGTGAAGCGCTGGAACTCACTCGAGTCCAGTG 2700  
Db 2826 TATTTTGGAAACGTCAGAGATGTGAAGCGCTGGAACTCACTCGAGTCCAGTG 2885  
Qy 2701 TTTTCCCACTGTCACTCTCTCCAGGGCTCTGGACCCTCCGGCATCAAAAGCAGAA 2760  
Db 2886 TTTTCCCACTGTCACTCTCTCCAGGGCTCTGGACCCTCCGGCATCAAAAGCAGAA 2945  
Qy 2761 GAGAGGTGTGAGAACTGTTTGATGACACACAGGATTTTACATTCAGAGGCTTGGTCTTGTG 2820  
Db 2946 GAGAGGTGTGAGAACTGTTTGATGACACACAGGATTTTACATTCAGAGGCTTGGTCTTGTG 3005  
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Db 3006 TTTTGGAAACGTCGCGTGGTTCGCGTCTGAGTCCAGTCTGAGGATTTGTC 3065  
Qy 2881 ATCATCGTTGCTTGGTGGTCTGATCTCGCAAAACCTCTGGATCCGGCGAGTGGT 2940  
Db 3066 ATCATCGTTGCTTGGTGGTCTGATCTCGCAAAACCTCTGGATCCGGCGAGTGGT 3125  
Qy 2941 TTGGCACTGCTCTATGCCCTCACGCTCATAGGGATGTTTCAGTGGTGTGTTTCGACAAAGT 3000  
Db 3126 TTGGCACTGCTCTATGCCCTCACGCTCATAGGGATGTTTCAGTGGTGTGTTTCGACAAAGT 3185  
Qy 3001 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAGGGTCATTTGAATACACAGACTTGAA 3060  
Db 3186 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAGGGTCATTTGAATACACAGACTTGAA 3245  
Qy 3061 AAAGAGCACCTTGGAAATATCAGAAAGCCCAACACAGGCTGGCCCATGAGGAGTG 3120  
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Qy 3121 ATAACTTTTGAATGTGAACCTTCATGTACAGTCCAGTGGGCTCTGTGTACTGAAGCAT 3180  
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Qy 3181 CTGACAGCACTCATTTAAATCAAGAAAGGTTGGCAATTTGGGAAGAACCCGAGCTGGA 3240  
Db 3366 CTGACAGCACTCATTTAAATCAAGAAAGGTTGGCAATTTGGGAAGAACCCGAGCTGGA 3425  
Qy 3241 AAAAGTCCCTCATCTAGCCCTTTTATAGATTGTGAGAACCCGAGGATTAATTTGGATT 3300  
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Qy 3301 GATAAGATCTTGACAACTGAAATTTGGAATTCACGATTTTAAAGAAAGAAATGTCATATCATA 3360  
Db 3486 GATAAGATCTTGACAACTGAAATTTGGAATTCACGATTTTAAAGAAAGAAATGTCATATCATA 3545  
Qy 3361 CCTCAGGAACCTGTTTGTTCACCTGGAAACAATGAGGAAACCTTGGATCCCTTTTAAATGAG 3420

Db 3546 CCTCAGGAACCTGTTTGTTCACCTGGAAACAATGAGGAAAAACCTGGATCCCTTTTAAATGAG 3605  
Qy 3421 CACACGGATGAGGAACCTGTGGAATGCCTTTACAGAGGTACAACTTTAAAGAAACCACTTGAA 3480  
Db 3606 CACACGGATGAGGAACCTGTGGAATGCCTTTACAGAGGTACAACTTTAAAGAAACCACTTGAA 3665  
Qy 3481 GATCTTCTGTGTAATAATGGATACCTGAATTTAGCAGAACTCAGGATCCAATTTTGTAGTTCGA 3540  
Db 3666 GATCTTCTGTGTAATAATGGATACCTGAATTTAGCAGAACTCAGGATCCAATTTTGTAGTTCGA 3725  
Qy 3541 CAAAGACAACTGGTGTGCTTCCAGGGCAATTTCTCAGAAAAATCAGATTTGATTTATT 3600  
Db 3726 CAAAGACAACTGGTGTGCTTCCAGGGCAATTTCTCAGAAAAATCAGATTTGATTTATT 3785  
Qy 3601 GATGAAGCGACGGCAATTTGATGATCCCAAGAACTGATGATTAATAACAAAAAATCCGG 3660  
Db 3786 GATGAAGCGACGGCAATTTGATGATCCCAAGAACTGATGATTAATAACAAAAAATCCGG 3844  
Qy 3661 GAGAAATTTGCCACTGCTCACCGTCTAACCAATGTCACACAGATTGAACCACTTATTTGAC 3720  
Db 3845 GAGAAATTTGCCACTGCTCACCGTCTAACCAATGTCACACAGATTGAACCACTTATTTGAC 3904  
Qy 3721 AGCGACAAAGATTAATGGTGTGATTTAGATTTAGGAAAGCTGAAAGAAATATGATGAGCCGTATGTT 3780  
Db 3905 AGCGACAAAGATTAATGGTGTGATTTAGATTTAGGAAAGCTGAAAGAAATATGATGAGCCGTATGTT 3964  
Qy 3781 TTGCTGCAAAATAAGAGAGCTTATTTTACAGATGGTCAACCACTGGCAAGGACAGAA 3840  
Db 3965 TTGCTGCAAAATAAGAGAGCTTATTTTACAGATGGTCAACCACTGGCAAGGACAGAA 4024  
Qy 3841 GCCCTGCCCTCTACTGAAACAGCAAAACAGGATATATCTTCAAAAGAAATTTATCCACATATT 3900  
Db 4025 GCCCTGCCCTCTACTGAAACAGCAAAACAGGATATATCTTCAAAAGAAATTTATCCACATATT 4084  
Qy 3901 GGTCACTGACCACTGTTTACAAACACTTCCAAATGAGAGCCCTCGACCTTAACTATT 3960  
Db 4085 GGTCACTGACCACTGTTTACAAACACTTCCAAATGAGAGCCCTCGACCTTAACTATT 4144  
Qy 3961 TTCAGAGACGACCTGTGA 3978  
Db 4145 TTCAGAGACGACCTGTGA 4162

## RESULT 15

AA563921  
ID AA563921 standard; cdna; 6082 BP.  
XX  
AC AA563921;  
XX  
DT 29-JAN-2002 (first entry)  
XX  
DE Human prostate cDNA sequence #438.  
XX  
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200173032-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 27-MAR-2001; 2001WO-US009919.  
XX  
PR 27-MAR-2000; 2000US-00536857.  
PR 09-MAY-2000; 2000US-00568100.  
PR 12-MAY-2000; 2000US-00570737.  
PR 13-JUN-2000; 2000US-00593793.  
PR 27-JUN-2000; 2000US-00605783.  
PR 09-AUG-2000; 2000US-00636215.  
PR 29-AUG-2000; 2000US-00651236.  
PR 06-SEP-2000; 2000US-00657279.  
PR 02-OCT-2000; 2000US-00679426.  
PR 10-OCT-2000; 2000US-00685166.



PR 09-NOV-2000; 2000US-00709729.  
XX (CORI-) CORIXA CORP.  
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;  
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;  
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;  
XX WPI; 2001-639232/73.  
DR P-PSDB; AAU69823.  
XX New human prostate-specific polypeptides and polynucleotides useful for  
PT the diagnosis and treatment of cancer, especially prostate cancer.  
XX  
PS Claim 1; Page 410-412; 579pp; English.  
XX  
CC The invention relates to isolated prostate-specific polynucleotides,  
CC polypeptides, fusion proteins of the polypeptides, antibodies raised  
CC against the polypeptides (or antigenic epitopes derived from them) and  
CC antigen-presenting cells expressing the polypeptides. The antibodies are  
CC useful for detecting the presence of cancer, especially prostate cancer.  
CC The polypeptides, polynucleotides and the antigen-presenting cells are  
CC useful for stimulating and/or expanding T cells specific for a tumour  
CC protein, and for inhibiting the development of cancer especially prostate  
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are  
CC useful for stimulating an immune response, and for treating cancer. The  
CC oligonucleotide is useful for detecting cancer. The present sequence is a  
CC prostate specific polynucleotide of the invention  
XX  
SQ Sequence 6082 BP; 1721 A; 1249 C; 1357 G; 1755 T; 0 U; 0 Other;  
  
Query March 99.7%; Score 3966; DB 4; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
Qy 1 ATGCTGCCCGTGACACGAGGTGAAGCCCAACCGCTGCAGGACGGAACTCTGCTCA 60  
Db 186 ATGCTGCCCGTGACACGAGGTGAAGCCCAACCGCTGCAGGACGGAACTCTGCTCA 245  
  
Qy 61 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTGTTTAAATTTGGCCATAAACGGAGATTAG 120  
Db 246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTGTTTAAATTTGGCCATAAACGGAGATTAG 305  
  
Qy 121 GAAGATGATATGATTTCAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGATTG 180  
Db 306 GAAGATGATATGATTTCAGTGCTGCCAGAGACCGCTCACAGCACCTTGGAGAGATTG 365  
  
Qy 181 CAAGGTTCTGGGATAAAGATTGTTAAGAGCTGAGATGACGACAGAACCTTCTTTA 240  
Db 366 CAAGGTTCTGGGATAAAGATTGTTAAGAGCTGAGATGACGACAGAACCTTCTTTA 425  
  
Qy 241 ACAAGAGCAATCATAAAGTGTTACTGGAATCTTTATTTAGTTTGGGAATTTTACGTTA 300  
Db 426 ACAAGAGCAATCATAAAGTGTTACTGGAATCTTTATTTAGTTTGGGAATTTTACGTTA 485  
  
Qy 301 ATTGAGGAAGTGCACAAAGTAATCCAGCCATATTTTGGGAAAAATTAATTAATTTT 360  
Db 486 ATTGAGGAAGTGCACAAAGTAATCCAGCCATATTTTGGGAAAAATTAATTAATTTT 545  
  
Qy 361 GAAATATATGATCCCATGATTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 420  
Db 546 GAAATATATGATCCCATGATTCTGTGGCTTTGAACACAGCGTACGCTATGCCACGGTG 605  
  
Qy 421 CTGACTTTTTCACGCTCAATTTGGCTATCTACTGCATCACTTATATTTTATFACGTTTCA 480  
Db 606 CTGACTTTTTCACGCTCAATTTGGCTATCTACTGCATCACTTATATTTTATFACGTTTCA 665  
  
Qy 481 TGTCTGGGATGAGTTACGATGAGCCATGTCATATGATTTATCGGAAGGCATTCGT 540  
Db 666 TGTCTGGGATGAGTTACGATGAGCCATGTCATATGATTTATCGGAAGGCATTCGT 725  
  
Qy 541 CTTAGTAAACATGGCCATGGGGAAGACACACACAGCCAGATAGTCAATCTCTGCTCCAAT 600  
Db 1865 GCACGGGTAAACCTTGCACAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1865

Db 726 CTTAGTAAACATGGCCATGGGGAAGACAAACACAGCCAGATAGTCAATCTGCTGTCCAAT 785  
Qy 601 GATGTGAACAAGTTTGNATCAGGTGACAGTCTTTTACACTTCTCTGTTGGGAGGACCACTG 660  
Db 786 GATGTGAACAAGTTTGNATCAGGTGACAGTCTTTTACACTTCTCTGTTGGGAGGACCACTG 845  
Qy 661 CAGCGCATCGCAGTACTGCTTACTCTGATGGAGATAGGAATATGCTGCTTGTCTGGG 720  
Db 846 CAGCGCATCGCAGTACTGCTTACTCTGATGGAGATAGGAATATGCTGCTTGTCTGGG 905  
Qy 721 ATGCGAGTTCTAATCAFTTCTCTGCTTCCAAAGCTGTTTGGGAAGTGTTCCTCATCA 780  
Db 906 ATGCGAGTTCTAATCAFTTCTCTGCTTCCAAAGCTGTTTGGGAAGTGTTCCTCATCA 965  
Qy 781 CTGAGGATGAAAACCTGCAACTTTTACGGATGCCAGGATCAGGACCATGAATGAATGATA 840  
Db 966 CTGAGGATGAAAACCTGCAACTTTTACGGATGCCAGGATCAGGACCATGAATGAATGATA 1025  
Qy 841 ACTGGTATAAGGATAATAAAAATGTCGCTGGGAAAAGTCATTTTCAAATCTTTATTACC 900  
Db 1026 ACTGGTATAAGGATAATAAAAATGTCGCTGGGAAAAGTCATTTTCAAATCTTTATTACC 1085  
Qy 901 AATTGTGAAAAGAGGAGATTTCAGATTTCTGAGAAAGTTCTGCTCCCTCAGGGGATGAAT 960  
Db 1086 AATTGTGAAAAGAGGAGATTTCAGATTTCTGAGAAAGTTCTGCTCCCTCAGGGGATGAAT 1145  
Qy 961 TTGGCTTGGTTTTTTCAGTGAAGCAAAATCATGCTGTTTGTGACCTTTCACCACCTACGTG 1020  
Db 1146 TTGGCTTGGTTTTTTCAGTGAAGCAAAATCATGCTGTTTGTGACCTTTCACCACCTACGTG 1205  
Qy 1021 CTCCTCGGCAGTGTGATCACAGCCAGCCGCTGTTCTGTCAGTGACGCTGTATGGGGCT 1080  
Db 1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCTGTTCTGTCAGTGACGCTGTATGGGGCT 1265  
Qy 1081 GTGCGGCTGACGTTTACCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1140  
Db 1266 GTGCGGCTGACGTTTACCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATC 1325  
Qy 1141 GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTTCATGAGATATCACAGCGCAACCGT 1200  
Db 1326 GTGAGCATCGAAGAAATCCAGACCTTTTGTCTACTTCATGAGATATCACAGCGCAACCGT 1385  
Qy 1201 CAGCTGCCGTGAGATGTTAAAGATGTTGTCATGTCAGGATTTTACTGCTTTTGGGAT 1260  
Db 1386 CAGCTGCCGTGAGATGTTAAAGATGTTGTCATGTCAGGATTTTACTGCTTTTGGGAT 1445  
Qy 1261 AAGCATCAGAGACCCCAACTCTACAAGGCTTTCTTTTACTGTGACAGCTGGCGAATG 1320  
Db 1446 AAGCATCAGAGACCCCAACTCTACAAGGCTTTCTTTTACTGTGACAGCTGGCGAATG 1505  
Qy 1321 TTAGCTGTGTCGGCCCGTGGGAGCAGGGAAGTCATCAGTGTAAAGTGGCGTCTCGGG 1380  
Db 1506 TTAGCTGTGTCGGCCCGTGGGAGCAGGGAAGTCATCAGTGTAAAGTGGCGTCTCGGG 1565  
Qy 1381 GAATTGSCCCCAAGTCACGSGCTGTCAGCGTGCATGGAAGAAATGCTATGTCTCAG 1440  
Db 1566 GAATTGSCCCCAAGTCACGSGCTGTCAGCGTGCATGGAAGAAATGCTATGTCTCAG 1625  
Qy 1441 CAGCCCTGGGTGTTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
Db 1626 CAGCCCTGGGTGTTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685  
Qy 1501 AAGGAACGATATGAAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTTG 1560  
Db 1686 AAGGAACGATATGAAAAAGTCATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTTG 1745  
Qy 1561 GAGGATGTTGATCTGATCTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAA 1620  
Db 1746 GAGGATGTTGATCTGATCTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAA 1805  
Qy 1621 GCACGGTAAACCTTGCACAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1680  
Db 1806 GCACGGTAAACCTTGCACAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1865

Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACATTGTTCCGAACCTGTGTATTGTCAA 1740  
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1686 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAA 1925  
Qy 1741 ATTTTGCATGAGAGATCACAAATTTTGTAGTGACTCATCATGTTGCGAGTACCTCAAGAGTCGCA 1800  
Db |||||  
1926 ATTTTGCATGAGAGATCACAAATTTTGTAGTGACTCATCATGTTGCGAGTACCTCAAGAGTCGCA 1985  
Qy 1801 AGTCAGATTTCTGATATTGAAGATGGTAAATGTGTGCAAGAGGAGACTTACACTGAGTTC 1860  
Db |||||  
1986 AGTCAGATTTCTGATATTGAAGATGGTAAATGTGTGCAAGAGGAGACTTACACTGAGTTC 2045  
Qy 1861 CTAAAAATCTGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGGAAAGTGAACAA 1920  
Db |||||  
2046 CTAAAAATCTGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGGAAAGTGAACAA 2105  
Qy 1921 CCTCCAGTCCAGGAATCCACACTAAGGAATCGTACTTCTCAGAGTCTTCGTTTGG 1980  
Db |||||  
2106 CCTCCAGTCCAGGAATCCACACTAAGGAATCGTACTTCTCAGAGTCTTCGTTTGG 2165  
Qy 1981 TCTCAACAATCTTCTAGACCTCTTGAAGATGCTGCTCGGAGAGCCAAAGATACAGAG 2040  
Db |||||  
2166 TCTCAACAATCTTCTAGACCTCTTGAAGATGCTGCTCGGAGAGCCAAAGATACAGAG 2225  
Qy 2041 AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCC 2100  
Db |||||  
2226 AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCC 2285  
Qy 2101 TATAAGAAATTTACTCAGAGCTGGTGCTCATCTGGAATGTCTTCATTTTCTTCTCTTA 2160  
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2286 TATAAGAAATTTACTCAGAGCTGGTGCTCATCTGGAATGTCTTCATTTTCTTCTCTTA 2345  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGCTTTCATCTGGGCAAC 2220  
Db |||||  
2346 AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGCTTTCATCTGGGCAAC 2405  
Qy 2221 AACAAAGATATGCTAAATGTCACTGTAAATGAGGAGGAAATGTAAACCGAGAAGCTAGAT 2280  
Db |||||  
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Qy 2281 CTTAACTGGTACTTAGGAATTTTATCAGGTTTAACTGTAGTACCGTTCTTTTGGCATA 2340  
Db |||||  
2466 CTTAACTGGTACTTAGGAATTTTATCAGGTTTAACTGTAGTACCGTTCTTTTGGCATA 2525  
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Db |||||  
2526 GCAAGATCTCTATTGGTATTCTACGTCCTCTGTTAACTCTTACACAACTTTGCAACAAA 2585  
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2586 ATGTTTTCAGTCAATTTCTGAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645  
Qy 2461 ATTTTAAATCGTTTCTCAAAGACATTTGGACATCTTGGAGATTTGCTGCCGCTGACGTTT 2520  
Db |||||  
2646 ATTTTAAATCGTTTCTCAAAGACATTTGGACATCTTGGAGATTTGCTGCCGCTGACGTTT 2705  
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Db |||||  
2766 ATTCTTTGGATTCGAATACCTCTGGTTCCCTCTGGAATCATTTTTCATTTTCTTCCGCGA 2825  
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Qy 2761 GAGAGGTGTGAGGAACTGTTTGTATGTCACACAGGATTTTACATTCAGAGGCTTGGTTCTTG 2820  
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Qy 2821 TTTTGTGACAGCTCCCGTGGTTCCGCTCGGTCTGATGCGCATCTGTGCCATGTTTGTGTC 2880  
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3186 GCTGAGCTTCAGATATGATGATCTCAGTGAAGAGGTCATTGTAATACACAGACCTTGAA 3245  
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3246 AAAGAACACCTTGGGAATATCAGAAACGCCACACAGCTGCGCCCATGAAGAGAGTG 3305  
Qy 3121 ATAATCTTTGACAAATGTGAACCTTCATCTACGTCCAGGTGGGCTCTGTTACTGAAGCAT 3180  
Db |||||  
3306 ATAATCTTTGACAAATGTGAACCTTCATCTACGTCCAGGTGGGCTCTGTTACTGAAGCAT 3365  
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Db |||||  
3366 CTGACGACCTCATTAAATCACAAGAAAGGTTGGCAATTTGGGAAAGAACCGGAGCTGGA 3425  
Qy 3241 AAAAGTTCCCTCATCTCAGGCCCTTTTAGATTTGTGAGAACCCGGAAGGTAATAATTTGGATT 3300  
Db |||||  
3426 AAAAGTTCCCTCATCTCAGGCCCTTTTAGATTTGTGAGAACCCGGAAGGTAATAATTTGGATT 3485  
Qy 3301 GATAAGATCTTGACAACTGAAATTTGACCTTCAAGATTTAAGGAAGAAATGTCAATCATA 3360  
Db |||||  
3486 GATAAGATCTTGACAACTGAAATTTGACCTTCAAGATTTAAGGAAGAAATGTCAATCATA 3545  
Qy 3361 CCTCAGGAACTGTTTGTTCACCTGGAACCAATGAGGAAACCTTGGATCCCTTTAATGAG 3420  
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3546 CCTCAGGAACTGTTTGTTCACCTGGAACCAATGAGGAAACCTTGGATCCCTTTAATGAG 3605  
Qy 3421 CACACGATCAGGAACTGTGGAATGCTTACAAGAGGTACAACCTTAAAGAAACCATTGAA 3480  
Db |||||  
3606 CACACGATCAGGAACTGTGGAATGCTTACAAGAGGTACAACCTTAAAGAAACCATTGAA 3665  
Qy 3481 GATCTTCTCGTAAAAATGGATCTGAATTTAGCAGAAATCAGGATCCAAATTTTGTGTTGGA 3540  
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3666 GATCTTCTCGTAAAAATGGATCTGAATTTAGCAGAAATCAGGATCCAAATTTTGTGTTGGA 3725  
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Db |||||  
3726 CAAAGACAACTGGTGTGCTTGCAGGGCAATTTCTCAGGAAACCAATCAGATATTGATTTATT 3785  
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3786 GATGAAGCGAGCGCAATGTGGATFCCAAAGAACTGATGAGTTTAAATAC-AAAAAATAATCCGG 3844  
Qy 3661 GAGAAATTTGCCCACTGACCGTGTAAACCAATTTGACACAGATTTGAACACCATTTATTGAC 3720  
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3845 GAGAAATTTGCCCACTGACCGTGTAAACCAATTTGACACAGATTTGAACACCATTTATTGAC 3904  
Qy 3721 AGCGACAAGATTAATGTTTTAGATTTAGGAGACTGAAAGAAATATGATGAGCCGTATGTT 3780  
Db |||||  
3905 AGCGACAAGATTAATGTTTTAGATTTAGGAGACTGAAAGAAATATGATGAGCCGTATGTT 3964  
Qy 3781 TTGCTGCAAAATAAAGAGAGCTTATTTTACAAGATGTGCAACAACTGGGCAAGCGAGAA 3840  
Db |||||  
3965 TTGCTGCAAAATAAAGAGAGCTTATTTTACAAGATGTGCAACAACTGGGCAAGCGAGAA 4024  
Qy 3841 GCGCTGCCCTCACTGAAACACAGCAAAACAGGTATATTCTCAAAAGAAATTTATCCACATATT 3900

[illegible]

Search completed: May 20, 2005, 04:30:37  
Job time : 1997 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2005, 03:46:56 ; Search time 2476 Seconds  
(without alignments)  
9852.332 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcgcgtgtaccagga.....tttccgagacgacgtgtga 3978

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3978	100.0	3978	17	US-10-295-027-569
2	3973.2	99.9	4231	10	US-09-930-213-287
3	3973.2	99.9	4231	17	US-10-295-027-571
4	3973.2	99.9	4231	19	US-10-889-503-1
5	3973.2	99.9	5870	15	US-10-205-823-1
6	3973.2	99.9	5871	19	US-10-887-553A-717
7	3966	99.7	6082	9	US-09-759-143-535
8	3966	99.7	6082	9	US-09-780-669-535
9	3966	99.7	6082	9	US-09-822-827-535
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## ALIGNMENTS

### RESULT 1

US-10-295-027-569  
; Sequence 569, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynn, Richard  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; FILE REFERENCE: 018501-012500US  
; CURRENT APPLICATION NUMBER: US/10/295,027  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/350,666  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,394  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/332,464  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/347,211  
; PRIOR FILING DATE: 2002-01-08

ABR

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; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 569
; LENGTH: 3978
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-569

Query Match      100.0%; Score 3978; DB 17; Length 3978;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 GAAGATGATATGATTTCAGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180

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Db	2941	TTGGCACTG	CTCTATG	CCCTCA	CGCTCAT	GGGAGT	TTTT	CAGTGG	TGTGTTGCACAAAGT 3000

RESULT 2  
US-09-930-213-287  
; Sequence 287, Application US/09930213  
; Publication No. US20030170625A1

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; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERNHARD
; APPLICANT: SCHAFFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHE-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELNIGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SEKS, CHRISTINE
; FILE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930.213
; CURRENT FILING DATE: 2001-01-31
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 287
; LENGTH: 4231
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-930-213-287

Query Match      99.9%; Score 3973.2; DB 10; Length 4231;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 176 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAG 235

Qy 121 GAACATGATATGATTCAGTGTCTCCAGAGAGCCGCTCACAGCACCTTTGGAGAGAGTTG 180
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Db 356 ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 415

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Db 416 ATTCAGGAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAAAATTTATTAATTTT 475

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Db 476 GAAATATATGATCCATGGAATTCCTGGCTTTTGAACACAGCGTACGCTATGCCACGGTG 535

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Qy 1321 TTAGCTGTGTGCGCCCGCGGGAGCAGGAGGATCATCACTGTTAACTGCGCTCTCGG 1380
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Db 1796 CCTCTCAGTGCAGTAGATGCGGAGTTAGCAGACACTTGTTCGAACTGTGTTTGTCAA 1855
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RESULT 3  
US-10-295-027-571  
; Sequence 571, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
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; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
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; CURRENT APPLICATION NUMBER: US/10/295,027  
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; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2000-09-15  
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; PRIOR APPLICATION NUMBER: US 60/335,394  
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; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
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; PRIOR APPLICATION NUMBER: US 60/356,714  
; PRIOR FILING DATE: 2002-02-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 571  
; LENGTH: 4231  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-295-027-571

Query Match 99.9%; Score 3973.2; DB 17; Length 4231;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 3956 GCCCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 4015  
 Qy 3901 GGTCACTGACACATGGTTTACAAACACTTCCAAATGAGACGCCCTGACCTTAACTATT 3960  
 Db 4016 GGTCACTGACACATGGTTTACAAACACTTCCAAATGAGACGCCCTGACCTTAACTATT 4075  
 Qy 3961 TTCGAGACAGCAGTGTGA 3978  
 Db 4076 TTCGAGACAGCAGTGTGA 4093

RESULT 4

US-10-889-503-1  
 ; Sequence 1, Application US/10889503  
 ; Publication No. US20050063968A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fox Chase Cancer Center  
 ; APPLICANT: Kruh, Gary D.  
 ; APPLICANT: Lee, Kun  
 ; APPLICANT: Belinsky, Martin G.  
 ; APPLICANT: Bain, Lisa J.  
 ; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding  
 ; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof  
 ; FILE REFERENCE: FCCC 98-02  
 ; CURRENT APPLICATION NUMBER: US/10/889,503  
 ; CURRENT FILING DATE: 2004-07-12  
 ; PRIOR APPLICATION NUMBER: US/09/647,140  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US99/06644  
 ; PRIOR FILING DATE: 1999-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079,759  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/095,153  
 ; PRIOR FILING DATE: 1998-08-03  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4231  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-889-503-1

Query Match 99.9%; Score 3973.2; DB 19; Length 4231;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 ATGCTGCCGTGTACCAAGAGGTGAAGCCCAACCGCTGACAGGACGGAACTCTGCTCA 60  
 Db 116 ATGCTGCCGTGTACCAAGAGGTGAAGCCCAACCGCTGACAGGACGGAACTCTGCTCA 175

Qy 61 CGCGTGTCTTCTGCTGGCTCAATCCCTTCTTTAAATTTGCCCCATAAATCGGAGATTAGAG 120  
 Db 176 CGCGTGTCTTCTGCTGGCTCAATCCCTTCTTTAAATTTGCCCCATAAATCGGAGATTAGAG 235  
 Qy 121 GAAGATGATATGATATTCAGTGGCTGCCAAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 180  
 Db 236 GAAGATGATATGATATTCAGTGGCTGCCAAGAGACCGCTCACAGCACCTTGGAGAGAGTTG 295  
 Qy 181 CAAGGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGCACAGAGAGCTTCTTTA 240  
 Db 296 CAAGGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGCACAGAGAGCTTCTTTA 355  
 Qy 241 ACAAGAGCAATCATTAAGTCTTACTGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300  
 Db 356 ACAAGAGCAATCATTAAGTCTTACTGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 415  
 Qy 301 ATTGAGAAAAGTGCAAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTT 360  
 Db 416 ATTGAGAAAAGTGCAAAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTT 475  
 Qy 361 GAAAAATPATCATCCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCTATGCCAGGTG 420  
 Db 476 GAAAAATPATCATCCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCTATGCCAGGTG 535  
 Qy 421 CTGACTTTTTCACGCTCATTTTGGCTATCTGCATCACTTATATTTTATCACTTCACTG 480  
 Db 536 CTGACTTTTTCACGCTCATTTTGGCTATCTGCATCACTTATATTTTATCACTTCACTG 595  
 Qy 481 TGTGCTGGGATGAGTTTACGAGTAGCCATGTCGCATATGATTTATCGGAAAGGCACTTCGT 540  
 Db 596 TGTGCTGGGATGAGTTTACGAGTAGCCATGTCGCATATGATTTATCGGAAAGGCACTTCGT 655  
 Qy 541 CTTAGTAACATGGCCATGGGGAAGACAAACACAGGCCAGATGATCAATCTGCTGTCAAT 600  
 Db 656 CTTAGTAACATGGCCATGGGGAAGACAAACACAGGCCAGATGATCAATCTGCTGTCAAT 715  
 Qy 601 GATGTGAACAGTTTGAATCAGGTGACAGTCTTCTTACACTTCTGCTGGGAGGACCACTG 660  
 Db 716 GATGTGAACAGTTTGAATCAGGTGACAGTCTTCTTACACTTCTGCTGGGAGGACCACTG 775  
 Qy 661 CAGCGATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGTCTGCTGGG 720  
 Db 776 CAGCGATCGCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGTCTGCTGGG 835  
 Qy 721 ATGECAGTTCTAATCATTTCTGCTGCCCTTGAAAGCTGTTTGGGAAGTTGTTCTCATCA 780  
 Db 836 ATGECAGTTCTAATCATTTCTGCTGCCCTTGAAAGCTGTTTGGGAAGTTGTTCTCATCA 895  
 Qy 781 CTGAGGAGTAAACTGCAACTTTTACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840  
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 Qy 841 ACTGGTATAAGGATATAAAAAATGTCGCTGGGAAAGTCATTTTCAAAATCTTTATACC 900  
 Db 956 ACTGGTATAAGGATATAAAAAATGTCGCTGGGAAAGTCATTTTCAAAATCTTTATACC 1015  
 Qy 901 AATTGGAAGAAGGAGATTTCAGAAATCTGAGAAAGTTCTGCTGCCCTCAGGGGATGAAT 960  
 Db 1016 AATTGGAAGAAGGAGATTTCAGAAATCTGAGAAAGTTCTGCTGCCCTCAGGGGATGAAT 1075  
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 Db 1076 TTGGCTTCTGTTTTCAGTGCAGCAAAATCATCGTGTGTTGACCTTCCACCCTACGTG 1135  
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 Db 1136 CTCCTCGGAGTGTGATCACAGCCAGCCGGTGTTCGTGGCAGTGACGCTGTATGGGCT 1195  
 Qy 1081 GTGCGGCTGACGGTTACCTTCTTCCCTCAGCCATTTGAGAGGGTGTTCAGAGGCAATC 1140  
 Db 1196 GTGCGGCTGACGGTTACCTTCTTCCCTCAGCCATTTGAGAGGGTGTTCAGAGGCAATC 1255

QY 1141 GTCAGCATCCAGAAATCCAGACCTTTTGTCTACTTGTAGATAGATATACACAGCGAACCGT 1200  
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QY 1201 CAGCTGCCGTGAGATGTTAAAGATGTCATGTCAGAGGATTTACTGCTTTTGGAT 1260  
Db 1316 CAGCTGCCGTGAGATGTTAAAGATGTCATGTCAGAGGATTTACTGCTTTTGGAT 1375  
QY 1261 AAGGCATCAGAGACCCCAACTCTCAAGGCCCTTTCTTTTACTGTGTCAGACCTGGCGAATTG 1320  
Db 1376 AAGGCATCAGAGACCCCAACTCTCAAGGCCCTTTCTTTTACTGTGTCAGACCTGGCGAATTG 1435  
QY 1321 TTACTGTGTCGCCGCCCGTGGAGAGAGGAAATCATCACTGTTAAAGTGCCTGTCGG 1380  
Db 1436 TTACTGTGTCGCCGCCCGTGGAGAGAGGAAATCATCACTGTTAAAGTGCCTGTCGG 1495  
QY 1381 GAATTTGCCCAACTCAAGGCCCTGTCAGCGTGCATGGAAGATTTGCTATGTCCTCAG 1440  
Db 1496 GAATTTGCCCAACTCAAGGCCCTGTCAGCGTGCATGGAAGATTTGCTATGTCCTCAG 1555  
QY 1441 CAGCCCTGGGTGTTCTCGGGAATCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGAA 1500  
Db 1556 CAGCCCTGGGTGTTCTCGGGAATCTGAGGAGTAAATATTTTATTTGGGAAGAAATAGAA 1615  
QY 1501 AAGGAACGATATGAAAAGTCAAAAGCTTGTCTCTGAAAAGGATTTACAGCTGTTG 1560  
Db 1616 AAGGAACGATATGAAAAGTCAAAAGCTTGTCTCTGAAAAGGATTTACAGCTGTTG 1675  
QY 1561 GAGGATGTCATCTGACCTGATAGGATCGGGGAACCGCTGAGTGGAGGCGAGAA 1620  
Db 1676 GAGGATGTCATCTGACCTGATAGGATCGGGGAACCGCTGAGTGGAGGCGAGAA 1735  
QY 1621 GCAGGGTAAACCTTGAAGAGAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1680  
Db 1736 GCAGGGTAAACCTTGAAGAGAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1795  
QY 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTGTCGAACCTGTGATTTGCAA 1740  
Db 1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTGTCGAACCTGTGATTTGCAA 1855  
QY 1741 ATTTGTCATGAGAGATCACAATTTTATGATGATCTCATCAGTTGTCAGTACCTCAAGCTGCA 1800  
Db 1856 ATTTGTCATGAGAGATCACAATTTTATGATGATCTCATCAGTTGTCAGTACCTCAAGCTGCA 1915  
QY 1801 AGTCAGATTTCTGATTTGAAAGATGTTAAATGTCGAGAGGGGACTTACACTGAGTTC 1860  
Db 1916 AGTCAGATTTCTGATTTGAAAGATGTTAAATGTCGAGAGGGGACTTACACTGAGTTC 1975  
QY 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGAGGAAGTGAACAA 1920  
Db 1976 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGAGGAAGTGAACAA 2035  
QY 1921 CCTCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG 1980  
Db 2036 CCTCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG 2095  
QY 1981 TCTCAACAATCTCTAGACCTCTCTGAAAGATGTCCTCTGAGAGCCCAAGATACAGAG 2040  
Db 2096 TCTCAACAATCTCTAGACCTCTCTGAAAGATGTCCTCTGAGAGCCCAAGATACAGAG 2155  
QY 2041 AATGTCACAGTTACACTATCAGAGGAGAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCC 2100  
Db 2156 AATGTCACAGTTACACTATCAGAGGAGAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCC 2215  
QY 2101 TATAAGAAATTAATTCAGAGCTGGTCTCACTGGAATGTCCTTCAATTTTCTTATTTCTCCTA 2160  
Db 2216 TATAAGAAATTAATTCAGAGCTGGTCTCACTGGAATGTCCTTCAATTTTCTTATTTCTCCTA 2275  
QY 2161 AACACTCAGCTCAGGTTGCTATGTCCTCAAGATTTGTCGCTTCTACTGGGCAAC 2220  
Db 2276 AACACTCAGCTCAGGTTGCTATGTCCTCAAGATTTGTCGCTTCTACTGGGCAAC 2335  
QY 2221 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGAAATGTAAACCGAAGCTAGAT 2280

Db 2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGAAATGTAAACCGAAGCTAGAT 2395  
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Db 2396 CTTAACTGGTACTTTAGGAATTTATTTAGGTTTAACTGTAGCTACGTTCTTTTGGCATA 2455  
QY 2341 GCAAGATCTCTATTTGGTATTTCTACGTCCTTTAACTCTTTCACAAACTTTTCACAAACAA 2400  
Db 2456 GCAAGATCTCTATTTGGTATTTCTACGTCCTTTAACTCTTTCACAAACTTTTCACAAACAA 2515  
QY 2401 ATGTTTGAAGTCAATCTGAAAGCTCCGGTATTTATTTTGTATAGAAATCCAATAGGAAGA 2460  
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Db 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGAATGATTTGCTCCCGCTGACGTTT 2635  
QY 2521 TTAGATTTTCATCCACAGACATTTGCTACAAAGTGGTGGTGTCTCTGTGGCTGTGGCCGTG 2580  
Db 2636 TTAGATTTTCATCCACAGACATTTGCTACAAAGTGGTGGTGTCTCTGTGGCTGTGGCCGTG 2695  
QY 2581 ATTCTTTGGATTCGCAATACCTTGGTTCCTCTTGGAAATCATTTTTCATTTTCTTGGCGA 2640  
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QY 2641 TATTTTGGGAAGCTCAAGAGATGTCAGGCGCTGGAATCTCAACTCGAGGCTCCAGTG 2700  
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QY 2701 TTTTCCCACTTGTCACTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2760  
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QY 2761 GAGAGTGTGAGGAACCTGTTTGTATGACACACAGATTTTACATTGAGGCTTGTTCCTG 2820  
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QY 2821 TTTTGAACAAGCTCCCGCTGCTCGGTCCTGATGTCGATGCCATCTGTGCCATGTTTCTC 2880  
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Db 2996 ATCATCTGCTGCTTTGGGTCCTGATTTCTGGCAAAAACCTCTGGATGCCGGCAGGTTGGT 3055  
QY 2941 TTGGCACTGCTCTATGCCCTCAGCTCATGGGGATGTTTCAAGTGGTGTGTTTCGACAAAGT 3000  
Db 3056 TTGGCACTGCTCTATGCCCTCAGCTCATGGGGATGTTTCAAGTGGTGTGTTTCGACAAAGT 3115  
QY 3001 GCTGAAAGTTCAGATATGATGATCTCAGTAGAAGGCTCATTTGAATACACAGACCTTGAA 3060  
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QY 3061 AAAGAGCACTCTGGGAATATCAGAAAACCCACACAGCTGGCCCCCATGAAGGAGTG 3120  
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QY 3121 ATAATCTTTGACAAATGTGAACCTTCATGATCAGTCCAGGTGGGCTCTGTTGTTCTGAAGCAT 3180  
Db 3236 ATAATCTTTGACAAATGTGAACCTTCATGATCAGTCCAGGTGGGCTCTGTTGTTCTGAAGCAT 3295  
QY 3181 CTGACAGACTCATTAATCACAAGAAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3240  
Db 3296 CTGACAGACTCATTAATCACAAGAAAAGTTGGCAATTTGGGAAGAACCGGAGCTGGA 3355  
QY 3241 AAAAGTCCCTCATCTCAGGCCCTTTTGTAGATTTGTGAGAACCCGAAAGTAAATTTTGGATT 3300  
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Qy 3421 CACACGATGAGGAACCTGTTGAATGCTTACAGAGGTTACAACTTAAAGAAACCATTTGAA 3480  
Db 3536 CACACGATGAGGAACCTGTTGAATGCTTACAGAGGTTACAACTTAAAGAAACCATTTGAA 3595  
Qy 3481 GATCTTCTGTTAAATGGATCTGAAATAGCAGAAATCAGGATCCAAATTTTAGTGTGGA 3540  
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Db 3656 CAAAGACAACTGTTGCTTCCAGAGGCAATCTCAGGAAAAATCAGATATGATTAAT 3715  
Qy 3601 GATGACGACGCGCAAAATGTTGATCCAGAACTGATGAGTTAATACAAAAAATCCGG 3660  
Db 3716 GATGACGACGCGCAAAATGTTGATCCAGAACTGATGAGTTAATACAAAAAATCCGG 3775  
Qy 3661 GAGAAATTTGCCACTGACCGTCTAACCATTCACACAGATTTGAACACCATTTATTGAC 3720  
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Qy 3721 AGCACAAGATATGTTTTAGATTCAGGAAGACTGAAAGAAATATGATGAGCGGTATGTT 3780  
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Qy 3781 TTGCTGCAAAATAAGAGAGCTATTTTACAAGATGTTGCAACAACTGGCGCAGGCGAGAA 3840  
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Db 3956 GCCCTGCCCTCACTGAAACAGCAAAACAGGTATATCTTCAAAAGAAATTTCCACATATT 4015  
Qy 3901 GGTCACTAGCAGCATGTTTACAAACACTTCCAAATGAGAGCGCCTCGACCTTAACTATT 3960  
Db 4016 GGTCACTAGCAGCATGTTTACAAACACTTCCAAATGAGAGCGCCTCGACCTTAACTATT 4075  
Qy 3961 TTCGAGACAGCACTGTGA 3978  
Db 4076 TTCGAGACAGCACTGTGA 4093

## RESULT 5

US-10-205-823-1  
; Sequence 1, Application US/10205823  
; Publication No. US20030108963A1  
; GENERAL INFORMATION:  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Maniula  
; APPLICANT: Gorbacheva, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Wonsley, Angela M.  
; APPLICANT: Glatt, Karen  
; APPLICANT: Zhao, Xumei  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MRI-044  
; CURRENT APPLICATION NUMBER: US/10/205,823  
; PRIOR FILING DATE: 2002-07-25  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/341,746  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/362,158  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 5870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-205-823-1  
  
Query Match 99.9%; Score 3973.2; DB 15; Length 5870;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 ATGCTGCCCTGTACACAGGAGGTGAAGCCCAACCCCGCTGCAGGACGCGAACTCTGCTCA 60  
Db 116 ATGCTGCCCTGTACACAGGAGGTGAAGCCCAACCCCGCTGCAGGACGCGAACTCTGCTCA 175  
Qy 61 CGCGTGTCTTCTGCTGGCTCAATCCCTGTTTAAATTTGCCATAAACCGAGATTAGAG 120  
Db 176 CGCGTGTCTTCTGCTGGCTCAATCCCTGTTTAAATTTGCCATAAACCGAGATTAGAG 235  
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Qy 241 ACAAGCAATCATAAAGTCTTACTGAAATCTTATTTAGTTTGGAAATTTTTCAGTTA 300  
Db 356 ACAAGCAATCATAAAGTCTTACTGAAATCTTATTTAGTTTGGAAATTTTTCAGTTA 415  
Qy 301 ATTGAGAAAGTGCRAAGTAATCCAGCCCATATTTTGGGAAAAATATTAATTTT 360  
Db 416 ATTGAGAAAGTGCRAAGTAATCCAGCCCATATTTTGGGAAAAATATTAATTTT 475  
Qy 361 GAAAAATATGATCCCATGGATTCTGTGGCTTTGAAACAGCGTACGCTATGCCAGCGTG 420  
Db 476 GAAAAATATGATCCCATGGATTCTGTGGCTTTGAAACAGCGTACGCTATGCCAGCGTG 535  
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Qy 481 TGTGCTGGGATGAGTTTACGAGTAGCCATCTGCCATATGATTTATCGGAGGCACTTCGT 540  
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Qy 601 GATGTGAACAAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGAGGACCACTG 660  
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Qy 721 ATGGCAGTTCTTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAAGTTTCTTCATCA 780  
Db 836 ATGGCAGTTCTTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAAGTTTCTTCATCA 895  
Qy 781 CTGAGGAGTAAACTGCAATTTTCAACGATGCCAGGATCAGGACCATGAATGAAGTTATA 840  
Db 896 CTGAGGAGTAAACTGCAATTTTCAACGATGCCAGGATCAGGACCATGAATGAAGTTATA 955



Qy 841 ACTGGTATAAGGATAAATAAATGATACGCTTGGGAAAAGTCAATTTTCAAATCTTTATTACC 900  
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956 ACTGGTATAAGGATAAATAAATGATACGCTTGGGAAAAGTCAATTTTCAAATCTTTATTACC 1015  
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901 AATTTGAGAAAGAGAGATTTCAAGATCTCTGAGAGTTCCTGCCCTCAGGGGATGAAT 960  
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1016 AATTTGAGAAAGAGAGATTTCAAGATCTCTGAGAGTTCCTGCCCTCAGGGGATGAAT 1075  
Qy |||||  
961 TTGGCTTCGTTTTTTCAGTGCAGCAAAATCAATCGTTTGTGACCTTTCACCACTACGCTG 1020  
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1076 TTGGCTTCGTTTTTTCAGTGCAGCAAAATCAATCGTTTGTGACCTTTCACCACTACGCTG 1135  
Qy |||||  
1021 CTCCTCGCAGTGTGATCAAGCAGCGCGGTGTTCGTGGCAGTGAACGCTGTATGGGGCT 1080  
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1136 CTCCTCGCAGTGTGATCAAGCAGCGCGGTGTTCGTGGCAGTGAACGCTGTATGGGGCT 1195  
Qy |||||  
1081 GTGGGCTGACGGTTACCTCTTCTCCCTCAGCCATTCAGAGGTTGTCAGAGGCAATC 1140  
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1196 GTGGGCTGACGGTTACCTCTTCTCCCTCAGCCATTCAGAGGTTGTCAGAGGCAATC 1255  
Qy |||||  
1141 GTAGCATCCGAAGAACTCAGACCTTTTGTCTACTGTGATGAGATATCACAGCGCAACCGT 1200  
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1256 GTAGCATCCGAAGAACTCAGACCTTTTGTCTACTGTGATGAGATATCACAGCGCAACCGT 1315  
Qy |||||  
1201 CAGCTGCCGTGAGTGTAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGGAT 1260  
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1261 AAGGCATCAGAGACCCCACTCTACAGGCTTTCTTTACTGTGCAGACCTGGGGAATG 1320  
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1376 AAGGCATCAGAGACCCCACTCTACAGGCTTTCTTTACTGTGCAGACCTGGGGAATG 1435  
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1321 TTAGCTGTGTGCGGCCCGTGGAGCAGGGAAGTCATCACTGTTAACTGCGCTGCGG 1380  
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1436 TTAGCTGTGTGCGGCCCGTGGAGCAGGGAAGTCATCACTGTTAACTGCGCTGCGG 1495  
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1381 GAATTTGCCCCCAAGTCAAGGCTGGTGCAGCGTGCATGGAAGAAATGCTATGTCTCAG 1440  
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1496 GAATTTGCCCCCAAGTCAAGGCTGGTGCAGCGTGCATGGAAGAAATGCTATGTCTCAG 1555  
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1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTG 1560  
Db |||||  
1616 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTG 1675  
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1561 GAGGATGGTGATCTGACTGTATAGGAGATCGGGGAAACCGCTGAGTGGAGGGCAGAAA 1620  
Db |||||  
1676 GAGGATGGTGATCTGACTGTATAGGAGATCGGGGAAACCGCTGAGTGGAGGGCAGAAA 1735  
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1621 GCAGGGTAAACCTTGAAGAGCTGTATCAGATGCTGACATCTATCTCTGGAGCAT 1680  
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1796 CCTCTCAGTGCAGTGTAGTGCAGGAAATGATGAGACACTTGTTCGAACCTGTATTTGTCAA 1855  
Qy |||||  
1741 ATTTTGCATGAGAAGATCACAATTTTATGTAAGTGCAGTGTGAGTACCTCAAGCTGCA 1800  
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Qy |||||  
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1916 AGTCAGATCTGATATGAAAAGTGTGAAAATGATGAGAGGGAATTAACATGAGTTC 1975  
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1861 CTAATACTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAA 1920  
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1976 CTAATACTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAA 2035

Qy 1921 CCTCCAGTTCAGGAATCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980  
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2036 CCTCCAGTTCAGGAATCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095  
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1981 TCTCAACAATCTTCTAGACCTCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAG 2040  
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2156 AATGTCCCAAGTACACTATCAGAGGAAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215  
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2216 TATAAGAAATTAATTCAGAGCTGGTGTCTACTGTGATGTCTTTCATTTCTTTATTCCTTA 2275  
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Db 3836 AGCCACAAGATAATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3895
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Qy 3901 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 3960
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Db 4076 TTCGAGACAGCACTGTGA 4093

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RESULT 6  
 US-10-887-553A-717  
 ; Sequence 717, Application US/10887553A  
 ; Publication No. US20050085436A1  
 ; GENERAL INFORMATION:

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; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717
; LENGTH: 5871
; TYPE: DNA
; ORGANISM: human
; US-10-887-553A-717

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Query Match      99.9%; Score 3973.2; DB 19; Length 5871;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 121 GAAGATGATATGATTTACAGTGTGCCAGAAAGCCGCTCACAGCACCTTGGAGAGAGTTG 180
Db 236 GAAGATGATATGATTTACAGTGTGCCAGAAAGCCGCTCACAGCACCTTGGAGAGAGTTG 295
Qy 181 CAAGGGTCTGGGATAAAGAAAGTTTAAAGCTGAGATGACGACAGAGACCTTCTTTA 240
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Qy 421 CTGACTTTTTCACGCTCATTTTGGCTTATCTGCACTTATATTTTATACGTTTCAG 480
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Db 596 TGTGCTGGGATGAGTTTACGAGTAGCCATATGCCATATGATTTATCGGAAAGCACTTCGT 655
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Qy 601 GATCTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGCTGGGAGGACCACTG 660
Db 716 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGCTGGGAGGACCACTG 775
Qy 661 CAGCGCATCGCAGTACTGCCCTACTCTGAGTAGGATAGGAATATCGTGTGCTGGG 720
Db 776 CAGCGCATCGCAGTACTGCCCTACTCTGAGTAGGATAGGAATATCGTGTGCTGGG 835
Qy 721 ATGGCAGTTCTAATCATTTCTCGCCCTTCGAAAGCTGTTTGGGAAAGTTGTTCTCATCA 780
Db 836 ATGGCAGTTCTAATCATTTCTCGCCCTTCGAAAGCTGTTTGGGAAAGTTGTTCTCATCA 895

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Db	896	CTGAGGAGTAAAACTGCAACTTTTCA	CGGATGCCAGGATCAGGACATGAATGAAGTTATA	955
Qy	841	ACTGGTATAGGATTAATAAATCTAC	CGCTCGGAAAGTCAATTTCAATCTTATTACC	900
Db	956	ACTGGTATAGGATTAATAAATCTAC	CGCTCGGAAAGTCAATTTCAATCTTATTACC	1015
Qy	901	AAATTGAGAAAGAGAGATTTCCAA	GANTTCTGAGAAAGTTCCTGCCCTCAGGGGATGAAT	960
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Qy	961	TTGGCTTCGTTTTTTCAGTGCAGAA	CAAAATCATCGTTTGTGACCTTCAACACCTACGTTG	1020
Db	1076	TTGGCTTCGTTTTTTCAGTGCAGAA	CAAAATCATCGTTTGTGACCTTCAACACCTACGTTG	1135
Qy	1021	CTCCCTCGCGAGTGTGATCACAGC	CAGCGCGGTTCGTGGCAGTGACGCTGTATGGGGCT	1080
Db	1136	CTCCCTCGCGAGTGTGATCACAGC	CAGCGCGGTTCGTGGCAGTGACGCTGTATGGGGCT	1195
Qy	1081	GTGGGGCTGACGGTTACCCCTCTT	CTTCCCTCAGCCATTGAGAGGGTGTGACAGGGCAATC	1140
Db	1196	GTGGGGCTGACGGTTACCCCTCTT	CTTCCCTCAGCCATTGAGAGGGTGTGACAGGGCAATC	1255
Qy	1141	GTGAGCATCCGAAAGATCCAGACCT	TTTTTGTCTACTTGTATGATGATATCACAGCGCAACCGT	1200
Db	1256	GTGAGCATCCGAAAGATCCAGACCT	TTTTTGTCTACTTGTATGATGATATCACAGCGCAACCGT	1315
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Db	1316	CAGCTGCGGTGATGTGATTAAGAT	GTGTGATGTGATGAGGATTTTACTGCTTTTGGGAT	1375
Qy	1261	AAGGCATCAGAGACCCAACTCTCA	AGGCCCTTTTCTACTGTGACAGCTGGCGGAATTG	1320
Db	1376	AAGGCATCAGAGACCCAACTCTCA	AGGCCCTTTTCTACTGTGACAGCTGGCGGAATTG	1435
Qy	1321	TTAGCTGTGGTCCGCCCGTGGAG	CAAGGAGTCACTACTGTTTAAGTCCGCTCGGG	1380
Db	1436	TTAGCTGTGGTCCGCCCGTGGAG	CAAGGAGTCACTACTGTTTAAGTCCGCTCGGG	1495
Qy	1381	GAATTGGCCCCAGTCAAGGCTGGT	CAGCGTGTGATGGAAGATTTGCTGTCTCAG	1440
Db	1496	GAATTGGCCCCAGTCAAGGCTGGT	CAGCGTGTGATGGAAGATTTGCTGTCTCAG	1555
Qy	1441	CAGCCCTGGGTGTTCTCGGGAAC	TCTCAGGAGTAAATTTTATTTTGGGAAGAAATAGAA	1500
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Db	1676	GAGGATGGTGTACTGTGATAGGA	TAGGAGATCGGGGAACCGCTGAGTGGAGGGCAGAAA	1735
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Db	1736	GCAGGGTAAACCTTGAAGAGCAG	TGTATCAAGATCTGACATCTATCTCTGGAGCAT	1795
Qy	1681	CCTCTCAGTGCAGTAGATGCGAA	AGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA	1740
Db	1796	CCTCTCAGTGCAGTAGATGCGAA	AGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA	1855
Qy	1741	ATTTTGCATGAGAAAGATCACAA	TTTTTATGTAGTCACTCATCAGTTGCAAGTCTCAAAAGCTGCA	1800
Db	1856	ATTTTGCATGAGAAAGATCACAA	TTTTTATGTAGTCACTCATCAGTTGCAAGTCTCAAAAGCTGCA	1915
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Db	1916	AGTCAGATTTCTGATATTTGAAG	ATGGTAAATGTGACAGAGGGGACTTACACTGAGTTC	1975
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Db	1976	CTAAAACTCGGTATAGATTTTGG	CTCCCTTTTAAAGAAGGATAATGAGAAAGTGAACAA	2035
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Db	2036	CCTCCAGTTCAGGAACTCCACAC	TAAAGAACTCGTACCTTCTCAGAGTCTTCCGTTTGG	2095
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Db	2096	TCTCAACAAATCTTCTAGACCT	CTCTTGAAAGATGGTCTCTGGAGAGCAGAAATACAGAG	2155
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Db	2216	TATAAGAAATTTACTTTACAG	CTGGTCTCACTGGAATGTCTTTCAATTTCTTTATCTCTA	2275
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RESULT 7

, US-09-759-143-535

; Sequence 535, Application US/09759143  
; Patent No. US20020022248A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 535  
; LENGTH: 6082  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-759-143-535

Query Match 99.7%; Score 3966; DB 9; Length 6082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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## RESULT 8

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US-09-780-669-535
; Sequence 535, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 535
; TYPE: DNA
; LENGTH: 6082
; ORGANISM: Homo sapiens
US-09-780-669-535
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Query Match 99.7%; Score 3966; DB 9; Length 6082;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTTGGCTGCCGCTGACGTTT 2520
Db 2646 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTTGGCTGCCGCTGACGTTT 2705
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Db 2706 TTAGATTTTCATCCAGACATTTCTACAAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGCTG 2765
QY 2581 ATTCCCTTGGATCGCAATACCCCTTGGTTCCTCCCTTGGAAATCAATTTTCAATTTTCTTCGGCGA 2640
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QY 3121 ATAATCTTTGACAAATGGAATTCATGTACAGTCCAGGTGGCCCTCTGGTACTGAAGCAT 3180
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QY 3181 CTGACAGCATCTAATAATCACAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGA 3240
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Db 3905 AGCGACAAGATAATGTTTGTAGATTTCAAGGAAGTCTGAAGAAATATATGATGAGCCGTATGTT 3964
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Db 4145 TTCGAGACAGCACTGTGA 4162

RESULT 9
US-09-822-827-535
; Sequence 535, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-535

Query Match 99.7%; Score 3966; DB 9; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGCTGCCCTGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 60
Db 186 ATGCTGCCCTGTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245
QY 61 CGCGTGTCTTCTGCTGGCTCAATCCCTTGTTTAAATTCGCCATAACCGAGATTAGAG 120
Db 246 CGCGTGTCTTCTGCTGGCTCAATCCCTTGTTTAAATTCGCCATAACCGAGATTAGAG 305
QY 121 GAAGATGATATGATTCAGTGTGCTGCCAAGAAAGCCGCTCACAGCACCTTTGGAGGAGTTG 180
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QY 181 CAAGGGTTCGGGATAAAGAAAGTTTTHAAGCTGAGAAATCAGCACAAGAGCCCTTCTTTA 240
Db 366 CAAGGGTTCGGGATAAAGAAAGTTTTHAAGCTGAGAAATCAGCACAAGAGCCCTTCTTTA 425
QY 241 ACAAGACCAATCATAAAGTGTACTGGAATCTTATTAGTAAATTTTGGGAAATTTTACGTTA 300
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Qy ||||| 301 ATTGAGGAAGTGCACAAAGTAATCCAGGCCATATATTTTGGGAAAAATTAATAATTTATTTT 360  
Db ||||| 486 ATTGAGGAAGTGCACAAAGTAATCCAGGCCATATATTTTGGGAAAAATTAATAATTTATTTT 545  
Qy ||||| 361 GAAATATATGATCCCATCGATTTCTGTGGCTTTTGAAACACAGCGTACGCCCTATGCCACGGTG 420  
Db ||||| 546 GAAATATATGATCCCATCGATTTCTGTGGCTTTTGAAACACAGCGTACGCCCTATGCCACGGTG 605  
Qy ||||| 421 CTGACTTTTGGCAGCTCAATTTGGCTATATGCAATCACTTATATTTTATCACTTCAG 480  
Db ||||| 606 CTGACTTTTGGCAGCTCAATTTGGCTATATGCAATCACTTATATTTTATCACTTCAG 665  
Qy ||||| 481 TGTGCTGGGATGAGGTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCATCTCGT 540  
Db ||||| 666 TGTGCTGGGATGAGGTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCATCTCGT 725  
Qy ||||| 541 CTTAGTAAATGCGGCATGCGGAAGAACAAACACAGCCAGATGATCAATCTCTGTGCCAAT 600  
Db ||||| 726 CTTAGTAAATGCGGCATGCGGAAGAACAAACACAGCCAGATGATCAATCTCTGTGCCAAT 785  
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Qy ||||| 661 CAGGCGATCGCAGTGAAGTGCCTACTCTGAGTGGAGTAGGAATATCGTGTCTGTGGG 720  
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Qy ||||| 781 CTGAGGAGTAAATCTGCAACTTTTACCGATGCGAGGATCAGGACCATGAATGAAGTTATA 840  
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Qy ||||| 841 ACTGGTAAAGGATAAATAAATGTACCGCTGGGAAAGTCAATTTTCAAACTTTATTTACC 900  
Db ||||| 1026 ACTGGTAAAGGATAAATAAATGTACCGCTGGGAAAGTCAATTTTCAAACTTTATTTACC 1085  
Qy ||||| 901 AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAATTTCTGCTCAGGGGGATGAAT 960  
Db ||||| 1086 AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAATTTCTGCTCAGGGGGATGAAT 1145  
Qy ||||| 961 TTGGCTTCGTTTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCCACACCTACGTTG 1020  
Db ||||| 1146 TTGGCTTCGTTTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCCACACCTACGTTG 1205  
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Qy ||||| 1081 GTGGGCTGACGGTTACCGCTCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGCAATC 1140  
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Qy ||||| 1141 GTCAGCATCCGAGAAATCCAGACCTTTTGTGCTACTTGTATGATATCAACGCGAACCGT 1200  
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Qy ||||| 1201 CAGTGGCGTCAAGTGTGTAAGAGTGTGATGTCAGGAGTTTACTGCTTTTGGGAT 1260  
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Qy ||||| 1261 AAGGCATCAGAGACCCCAACTCTCAAGCCCTTTTCTTTTACTGTGTCAGACCTGGCGAATTG 1320  
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Qy ||||| 1321 TTAGCTGTGGTCCGCGCGTGGGAGCAGGGAAGTCATCACTGTTAAAGTCCGCTGCTCGGG 1380

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Db ||||| 1686 AAGGAACGATATGAAAGTCAATAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTG 1745  
Qy ||||| 1561 GAGGATGCTGATCTGCACTGTGATAGGAGATCGGGGAACACCGCTGAGTGGAGGCGAGAAA 1620  
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Qy ||||| 1621 GCACGGGTAAACCTTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGACGAT 1680  
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Qy ||||| 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGATTTGTCAA 1740  
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Qy ||||| 1801 AGTCAGATTTCTGATPATTGAAAGATGGTAAATATGGTGCAGAAAGGGGAACTTACACTGAGTTC 1860  
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Qy ||||| 2341 GCAAGATCTCTATTTGGTATTTCTAGCTCCTTGTAACTCTTCAAAAACCTTTGACAAACAAA 2400  
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 Db 4145 TTCGAGACGACACTGTGA 4162

RESULT 10

US-09-895-793-535  
 ; Sequence 535, Application US/09895793  
 ; Publication No. US20020192763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, JIANGCHUN  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqiu  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Rector, Marc W.  
 ; APPLICANT: Stolk, John H.  
 ; APPLICANT: Day, Craig H.  
 ; APPLICANT: Vedvick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Li, Samuel X.  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William T.  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Hural, John  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Houghton, Raymond L.  
 ; APPLICANT: Vinals de Baesols, Carlota  
 ; APPLICANT: Foy, Teresa  
 ; APPLICANT: Fanger, Gary R.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.534C2  
 ; CURRENT APPLICATION NUMBER: US/09/895,793  
 ; CURRENT FILING DATE: 2001-06-29  
 ; NUMBER OF SEQ ID NOS: 982  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 535  
 ; LENGTH: 6082  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-895-793-535

Query Match									
Best Local Similarity 99.7%; Score 3966; DB 9; Length 6082;									
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;									
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Qy	61	CGCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAATTTGCCATAAACGAGATTAGAG	120						
Db	246	CGCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAATTTGCCATAAACGAGATTAGAG	305						
Qy	121	GAAGATGATATGATTCAGTCTGCCAGAACCGCTCACAGCACCTTGGAGAGAGTTG	180						
Db	306	GAAGATGATATGATTCAGTCTGCCAGAACCGCTCACAGCACCTTGGAGAGAGTTG	365						
Qy	181	CAAGGTTCTGGGATAAGAGTTTAAAGCTGAGATGACGACAGAACCTTCTTTTA	240						
Db	366	CAAGGTTCTGGGATAAGAGTTTAAAGCTGAGATGACGACAGAACCTTCTTTTA	425						
Qy	241	ACAAGAGCAATCATAAAGTGTACTCGAAATCTTATTTAGTTTGGGAAATTTTACGTTA	300						
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Qy	301	ATTGAGGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT	360						
Db	486	ATTGAGGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT	545						
Qy	361	GAATAATTATGATCCCATGATCTGTGGCTTTGAACACAGGTTACGCTATGCCACGGT	420						
Db	546	GAATAATTATGATCCCATGATCTGTGGCTTTGAACACAGGTTACGCTATGCCACGGT	605						
Qy	421	CTGACTTTTTCAGCGCTCAATTTGGCTATCTGCAATCACTATATTTTATCAGTTTCAG	480						
Db	606	CTGACTTTTTCAGCGCTCAATTTGGCTATCTGCAATCACTATATTTTATCAGTTTCAG	665						
Qy	481	TGTGCTGGGATAGGTTACGATAGCCATGTCATATGATTTATCGAAAGGCACTTCGT	540						
Db	666	TGTGCTGGGATAGGTTACGATAGCCATGTCATATGATTTATCGAAAGGCACTTCGT	725						
Qy	541	CTTAGTAAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT	600						
Db	726	CTTAGTAAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT	785						
Qy	601	GATGTGAACAAGTTTGTATCAGTGCACAGTGTCTTACACTTCTGTCGGCAGGACCACTG	660						
Db	786	GATGTGAACAAGTTTGTATCAGTGCACAGTGTCTTACACTTCTGTCGGCAGGACCACTG	845						
Qy	661	CAGGCGATCGAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTCTTGTGGG	720						
Db	846	CAGGCGATCGAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTCTTGTGGG	905						
Qy	721	ATGGCAGTTCTAATCTCTGCTGCCCTTGGAAAGCTGTTTGGGAAAGTTGTTCTCATCA	780						
Db	906	ATGGCAGTTCTAATCTCTGCTGCCCTTGGAAAGCTGTTTGGGAAAGTTGTTCTCATCA	965						
Qy	781	CTGAGGAGTAAACCTGCAACTTTCACCGATGCCAGGATCAGGACCATGAATGAAGTTATA	840						
Db	966	CTGAGGAGTAAACCTGCAACTTTCACCGATGCCAGGATCAGGACCATGAATGAAGTTATA	1025						
Qy	841	ACTGGTATAAGGATAATAAAATGTACGCCCTGGGAAAGTCAATTTTCAAAATCTTATTAAC	900						
Db	1026	ACTGGTATAAGGATAATAAAATGTACGCCCTGGGAAAGTCAATTTTCAAAATCTTATTAAC	1085						
Qy	901	AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAAGTTCTGCTCCACAGGGGATGAAT	960						
Db	1086	AATTTGAGAAAGAGGAGATTTCAAGATTTCTGAGAAAGTTCTGCTCCACAGGGGATGAAT	1145						
Qy	961	TTGCTTTCGTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCCACCCACGTCGT	1020						
Db	1146	TTGCTTTCGTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCCACCCACGTCGT	1205						
Qy	1021	CTCCTCGGCAGTGTGATCACAGGCAGCGGTGTTCTGTCGGCAGTGCAGCTGTATGGGCT	1080						
1206		CTCCTCGGCAGTGTGATCACAGGCAGCGGTGTTCTGTCGGCAGTGCAGCTGTATGGGCT	1265						
1081		GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTCAGAGGCTGTCTAGAGCAATC	1140						
1266		GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTCAGAGGCTGTCTAGAGCAATC	1325						
1141		GTACAGCATCGAAGAAATCCAGACCTTTTGTCTACTTGTATGAGATATCACAGCGCAACCGT	1200						
1326		GTACAGCATCGAAGAAATCCAGACCTTTTGTCTACTTGTATGAGATATCACAGCGCAACCGT	1385						
1201		CAGCTGCCGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1260						
1386		CAGCTGCCGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1445						
1261		AAGGCATCAGAGACCCCAACTCTACAAAGGCTTTTCTTACTGTACAGACCTTGGGAAATG	1320						
1446		AAGGCATCAGAGACCCCAACTCTACAAAGGCTTTTCTTACTGTACAGACCTTGGGAAATG	1505						
1321		TTAGCTGTGGTCCGCCCTCGTGGAGCAGGGAAGTCACTCTGTTAAGTCCGCTGCTCGGG	1380						
1506		TTAGCTGTGGTCCGCCCTCGTGGAGCAGGGAAGTCACTCTGTTAAGTCCGCTGCTCGGG	1565						
1381		GAATTTGCCCTCAAGTCAACGGCTGGTTCAGGCTGATGGAAGAAATGCTATGTCTCAG	1440						
1566		GAATTTGCCCTCAAGTCAACGGCTGGTTCAGGCTGATGGAAGAAATGCTATGTCTCAG	1625						
1441		CAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAATATTTTATTTGGGAAAGAAATACGAA	1500						
1626		CAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAATATTTTATTTGGGAAAGAAATACGAA	1685						
1501		AAGGAAACGATATGAAAAGTCAAAAAGCTTTGCTCTGAAAAAGGATTTTACAGCTGTG	1560						
1686		AAGGAAACGATATGAAAAGTCAAAAAGCTTTGCTCTGAAAAAGGATTTTACAGCTGTG	1745						
1561		GAGGATGGTGTACTGCTGATGAGAGATCGGGGAAACCAAGCTGAGTGGAGGGCAGAAA	1620						
1746		GAGGATGGTGTACTGCTGATGAGAGATCGGGGAAACCAAGCTGAGTGGAGGGCAGAAA	1805						
1621		GCACGGGTAAACCTTGCACAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCAGAT	1680						
1806		GCACGGGTAAACCTTGCACAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCAGAT	1865						
1681		CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA	1740						
1866		CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTGTCAA	1925						
1741		ATTTTGCATGAGAAGATCAAAATTTTATGATGATCATCATCATCATCATCATCATCATCAT	1800						
1926		ATTTTGCATGAGAAGATCAAAATTTTATGATGATCATCATCATCATCATCATCATCATCAT	1985						
1801		AGTCAGATTTCTGATATTGAAGATGGTAAATTTGTCAGAGGGGACTTACACTGAGTTC	1860						
1986		AGTCAGATTTCTGATATTGAAGATGGTAAATTTGTCAGAGGGGACTTACACTGAGTTC	2045						
1861		CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAAAGATTAATGAGGAAAGTGAACAA	1920						
2046		CTAAATCTCGTATAGATTTTGGCTCCCTTTTAAAGAAAGATTAATGAGGAAAGTGAACAA	2105						
1921		CCTCCAGTTCAGGAACTCCCACTAAGGAAATGTTACCTTCTCAGAGTCTTCCGTTTGG	1980						
2106		CCTCCAGTTCAGGAACTCCCACTAAGGAAATGTTACCTTCTCAGAGTCTTCCGTTTGG	2165						
1981		TCTCAACAAATCTTCTAGACCTCTTGAAGATGGTGTCTCTGGAGAGCCCAAGATACAGAG	2040						
2166		TCTCAACAAATCTTCTAGACCTCTTGAAGATGGTGTCTCTGGAGAGCCCAAGATACAGAG	2225						
2041		AATGTCCAGTTACACTATCAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTTTCAGGCC	2100						
2226		AATGTCCAGTTACACTATCAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTTTCAGGCC	2285						
2101		TATAAGAAATTTCTCAGAGCTGGTGTCTACTGGAATGTTCTTCAATTTTCTTATTTCTCTTA	2160						

Db 2286 TATAAGAAATTACTTCAGAGCTGGTGCTCACTGGATTGCTTCATTTTCTTTATTTCTCCTA 2345  
Qy 2161 AACCTCAGCTCAGGTTCGTATATGCTCTCAAGATTGGTGGCTTCATATCACTCGGCGAAAC 2220  
Db 2346 AACACTCAGCTCAGGTTCGTATATGCTCTCAAGATTGGTGGCTTCATATCACTCGGCGAAAC 2405  
Qy 2221 AACAAAGTATGCTAAATGTCACGTGAATGAGGAGGAAATGTAACCGAGAGCTAGAT 2280  
Db 2406 AACAAAGTATGCTAAATGTCACGTGAATGAGGAGGAAATGTAACCGAGAGCTAGAT 2465  
Qy 2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2340  
Db 2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA 2525  
Qy 2341 GCAAGATCTCTATGTTGTAATCTAGTCTCTGTTTAACTCTTTCACAACTTTTGGCACAACAA 2400  
Db 2526 GCAAGATCTCTATGTTGTAATCTAGTCTCTGTTTAACTCTTTCACAACTTTTGGCACAACAA 2585  
Qy 2401 ATGTTTCAGTCAATCTCGAAAGCTCCGGTATTATTTCTTGATAGAAATCCAAATAGGAAGA 2460  
Db 2586 ATGTTTCAGTCAATCTCGAAAGCTCCGGTATTATTTCTTGATAGAAATCCAAATAGGAAGA 2645  
Qy 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGCGCTGACGTTT 2520  
Db 2646 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGCGCTGACGTTT 2705  
Qy 2521 TTAGATTTCAATCAGACATTTCTCAAGTGGTGGTGGTCTCTGTTGGCTGTGGCCGCTG 2580  
Db 2706 TTAGATTTCAATCAGACATTTCTCAAGTGGTGGTGGTCTCTGTTGGCTGTGGCCGCTG 2765  
Qy 2581 ATTCTTTGGATCGCAATACCTTGTTCCCTTGGAAATCATTTTTCATTTTCTTTCGCGGA 2640  
Db 2766 ATTCTTTGGATCGCAATACCTTGTTCCCTTGGAAATCATTTTTCATTTTCTTTCGCGGA 2825  
Qy 2641 TATTTTGTGAAACGCTCAAGAGATGTGAAGCGCTCGGAATCTCAACTCGGAGTCCAGTG 2700  
Db 2826 TATTTTGTGAAACGCTCAAGAGATGTGAAGCGCTCGGAATCTCAACTCGGAGTCCAGTG 2885  
Qy 2701 TTTTCCCACTTGTCATCTTCTCCAGGGGCTTGGAACATTCAGGCGATACAAAGCAGAA 2760  
Db 2886 TTTTCCCACTTGTCATCTTCTCCAGGGGCTTGGAACATTCAGGCGATACAAAGCAGAA 2945  
Qy 2761 GAGAGGTGTGAGGAACGTTTGTATGACACACAGGATTTACATTCAGAGGCTTGTTCTTG 2820  
Db 2946 GAGAGGTGTGAGGAACGTTTGTATGACACACAGGATTTACATTCAGAGGCTTGTTCTTG 3005  
Qy 2821 TTTTGTGACAACTGCTCCGCTGCTGCGCTCGGTCTGGATGCCATCTGTGCCATGTTTGTG 2880  
Db 3006 TTTTGTGACAACTGCTCCGCTGCTGCGCTCGGTCTGGATGCCATCTGTGCCATGTTTGTG 3065  
Qy 2881 ATCATCGTTGGCTTTGGGTCTCGATTCTTGCGCAAAATCTCTGGATGCGGGCAGGTTGGT 2940  
Db 3066 ATCATCGTTGGCTTTGGGTCTCGATTCTTGCGCAAAATCTCTGGATGCGGGCAGGTTGGT 3125  
Qy 2941 TTGGCACTGCTTATGCCCTCACGCTCATGGGATGTTTCAGTGGTGTGTTTCGACAAAGT 3000  
Db 3126 TTGGCACTGCTTATGCCCTCACGCTCATGGGATGTTTCAGTGGTGTGTTTCGACAAAGT 3185  
Qy 3001 GCTGAAAGTGTGAGATATGATGATCTCAGTAGAAAGGGTCAATTGAATACACAGACCTTGAA 3060  
Db 3186 GCTGAAAGTGTGAGATATGATGATCTCAGTAGAAAGGGTCAATTGAATACACAGACCTTGAA 3245  
Qy 3061 AAAGAAGCCTTTGGGAATATCAGAAACGCCACACACAGCTGGGCCCATGAAGAGGTG 3120  
Db 3246 AAAGAAGCCTTTGGGAATATCAGAAACGCCACACACAGCTGGGCCCATGAAGAGGTG 3305  
Qy 3121 ATAATCTTTGCAATGTGAATCTCATGTACAGTCCAGTGGGCTCTGTGTAATCTGAAGCAT 3180  
Db 3306 ATAATCTTTGCAATGTGAATCTCATGTACAGTCCAGTGGGCTCTGTGTAATCTGAAGCAT 3365  
Qy 3181 CTGACAGACTCATTTAAATCAAGAAAGGTTGGCATTTGTGGGAAGAACCGGAGCTGGA 3240  
Db 3366 CTGACAGACTCATTTAAATCAAGAAAGGTTGGCATTTGTGGGAAGAACCGGAGCTGGA 3425

Qy 3241 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTCTCAGAACCCGAGGTAAAATTTGGATT 3300  
Db 3426 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTCTCAGAACCCGAGGTAAAATTTGGATT 3485  
Qy 3301 GATAAGATCTTGACAACTGAAATTTGGACTTTCAGATTTTAAGGAAGAAAATGTCAATCATA 3360  
Db 3486 GATAGATCTTGACAACTGAAATTTGGACTTTCAGATTTTAAGGAAGAAAATGTCAATCATA 3545  
Qy 3361 CCTCAGGAACTGTTTGTTCACCTGGAACTGAGGAAAACTCTGGATCCCTTTAATAGAG 3420  
Db 3546 CCTCAGGAACTGTTTGTTCACCTGGAACTGAGGAAAACTCTGGATCCCTTTAATAGAG 3605  
Qy 3421 CACACGATGAGAACTGTGGATGCTTACAGAGGTACAACTTAAGGAAGAACCATTTGAA 3480  
Db 3606 CACACGATGAGAACTGTGGATGCTTACAGAGGTACAACTTAAGGAAGAACCATTTGAA 3665  
Qy 3481 GATCTTCTCGTAAATTTGGATCTGAATTAGCAGAACTCAGGATCCCAATTTTAGTGTGGA 3540  
Db 3666 GATCTTCTCGTAAATTTGGATCTGAATTAGCAGAACTCAGGATCCCAATTTTAGTGTGGA 3725  
Qy 3541 CAAAGCAACTGTGTGCTTTCAGGCAATTTCTCAGGAAAAATCAGATTTGATTTATT 3600  
Db 3726 CAAAGCAACTGTGTGCTTTCAGGCAATTTCTCAGGAAAAATCAGATTTGATTTATT 3785  
Qy 3601 GATGAGCGACGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGG 3660  
Db 3786 GATGAGCGACGCAATGTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGG 3844  
Qy 3661 GAGAAATTTCCCACTGACCGTGAACCATTTGCACACAGATTTGAAACCATTTATTGAC 3720  
Db 3845 GAGAAATTTCCCACTGACCGTGAACCATTTGCACACAGATTTGAAACCATTTATTGAC 3904  
Qy 3721 AGCGACAAGATAATGTTTGTAGATTCAGGAAGACTGAAAGATATGATGAGCCGTATGTT 3780  
Db 3905 AGCGACAAGATAATGTTTGTAGATTCAGGAAGACTGAAAGATATGATGAGCCGTATGTT 3964  
Qy 3781 TTCTCGCAAAATTAAGAGAGCCCTATTTTTCAAGATGTCACAACTGGCGCAAGGCGAGAA 3840  
Db 3965 TTCTCGCAAAATTAAGAGAGCCCTATTTTTCAAGATGTCACAACTGGCGCAAGGCGAGAA 4024  
Qy 3841 GCGCTGCCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 3900  
Db 4025 GCGCTGCCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATT 4084  
Qy 3901 GGTCACTCACTCAACATGTTTCAAAACATTTCCAAATGGAAGCCCTCGACCTTAACTATT 3960  
Db 4085 GGTCACTCACTCAACATGTTTCAAAACATTTCCAAATGGAAGCCCTCGACCTTAACTATT 4144  
Qy 3961 TTCGAGACGACACTGTGA 3978  
Db 4145 TTCGAGACGACACTGTGA 4162

## RESULT 11

US-09-895-814-535  
; Sequence 535, Application US/09895814  
; Publication No. US20020193296A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.

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; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C36
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-895-814-535

Query Match          99,7%; Score 3966; DB 9; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGCTGCCCGTGTACACGAGGTGAAGCCCAACCCGCTGCAGGACGGCAACCTCTGCTCA 60
Db 186 ATGCTGCCCGTGTACACGAGGTGAAGCCCAACCCGCTGCAGGACGGCAACCTCTGCTCA 245

Qy 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAG 120
Db 246 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTGTTAAATTTGGCCATAAACGGAGATTAGAG 305

Qy 121 GAAGATGATGATTTTCAAGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGATTG 180
Db 306 GAAGATGATGATTTTCAAGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGATTG 365

Qy 181 CAAGGGTCTCGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGACAGCCCTTCTTTA 240
Db 366 CAAGGGTCTCGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGACAGCCCTTCTTTA 425

Qy 241 ACAAGACAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 300
Db 426 ACAAGACAATCATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTA 485

Qy 301 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT 360
Db 486 ATTGAGAAAGTGCACAAAGTAATCCAGCCCATATTTTGGGAAATTTATTAATTTT 545

Qy 361 GAAATTTATGATCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCTATGCCCGGTG 420
Db 546 GAAATTTATGATCCATGGATTCTGTGGCTTTGAAACACAGCGTACGCTATGCCCGGTG 605

Qy 421 CTGACTTTTTCACGCTCATTTTGGCTATATCTGCATCACTTATTTTATCAGTTTCA 480
Db 606 CTGACTTTTTCACGCTCATTTTGGCTATATCTGCATCACTTATTTTATCAGTTTCA 665

Qy 481 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 540
Db 666 TGTGCTGGGATGAGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy 541 CTTAGTAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT 600
Db 726 CTTAGTAACATGGCCATGGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCCAAT 785

Qy 601 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGCTGGGAGGACCACTG 660
Db 786 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGCTGGGAGGACCACTG 845

Qy 661 CAGCGGATCCAGTGAATCTGCTGATGAGATGAGATATATCGTGCCTTGTGGG 720
Db 846 CAGCGGATCCAGTGAATCTGCTGATGAGATGAGATATATCGTGCCTTGTGGG 905

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Qy 721 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTTTGGGAAGTTGTTCTCATCA 780
Db 906 ATGCGAGTTCTAATCATTTCTCTGCCCTTGCAAGCTGTTTTTGGGAAGTTGTTCTCATCA 965

Qy 781 CTGAGGAGTAAACTGCAACTTTTACCGATGCGAGGATCAGGACCATGAATGAAGTTTATA 840
Db 966 CTGAGGAGTAAACTGCAACTTTTACCGATGCGAGGATCAGGACCATGAATGAAGTTTATA 1025

Qy 841 ACTGGTATAAGGATAAATAAAGTACGCTCGGCAAAAGTCATTTTCAAACTTTATTATACC 900
Db 1026 ACTGGTATAAGGATAAATAAAGTACGCTCGGCAAAAGTCATTTTCAAACTTTATTATACC 1085

Qy 901 AATTGAGAAAGAGGAGATTTCAGAGATTCTGAGAAAGTTCTCTCCCTCAGGGGAGTGAAT 960
Db 1086 AATTGAGAAAGAGGAGATTTCAGAGATTCTGAGAAAGTTCTCTCCCTCAGGGGAGTGAAT 1145

Qy 961 TTGGCTTCGTTTTTTCAGTGCAGCAAAATCATCTGTTTGTGACTTTCACCACTACGTTG 1020
Db 1146 TTGGCTTCGTTTTTTCAGTGCAGCAAAATCATCTGTTTGTGACTTTCACCACTACGTTG 1205

Qy 1021 CTCCTCGGCAGTGTGATCACAGCCAGCCGGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080
Db 1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy 1081 GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTTCAGAGGCAATC 1140
Db 1266 GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCCATTGAGAGGGTGTTCAGAGGCAATC 1325

Qy 1141 GTCAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGTATGAGATATCACAGCGCAACCGT 1200
Db 1326 GTCAGCATCCGAAGAATCCAGACCTTTTGTCTACTTGTATGAGATATCACAGCGCAACCGT 1385

Qy 1201 CAGTCGCCGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1386 CAGTCGCCGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1445

Qy 1261 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTACTGTCAGACCTTGGGCAATG 1320
Db 1446 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTACTGTCAGACCTTGGGCAATG 1505

Qy 1321 TTAGCTGTGTGGCCCGCTGGGAGCAGGGAAGTCACTGTTTAAAGTGCCTGCTCGGG 1380
Db 1506 TTAGCTGTGTGGCCCGCTGGGAGCAGGGAAGTCACTGTTTAAAGTGCCTGCTCGGG 1565

Qy 1381 GAATGGCCCAAGTCAACGGCTGTCAGCGTGCATGCAAGAAATTCCTATGCTCTCAG 1440
Db 1566 GAATGGCCCAAGTCAACGGCTGTCAGCGTGCATGCAAGAAATTCCTATGCTCTCAG 1625

Qy 1441 CAGCCCTGGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500
Db 1626 CAGCCCTGGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1560
Db 1686 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy 1561 GAGGATGTCATCTGACTGTGATAGGATCGGGGACCAAGCTGAGTGGAGGCGAGAA 1620
Db 1746 GAGGATGTCATCTGACTGTGATAGGATCGGGGACCAAGCTGAGTGGAGGCGAGAA 1805

Qy 1621 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1680
Db 1806 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGAT 1865

Qy 1681 CCTCTCAGTCAGTAGATCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740
Db 1866 CCTCTCAGTCAGTAGATCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy 1741 ATTTTGCATGAGAGATCACAAATTTTGTGACTCATCATGTTGCTGAGTACCTCAAGAGCTGCA 1800
Db 1926 ATTTTGCATGAGAGATCACAAATTTTGTGACTCATCATGTTGCTGAGTACCTCAAGAGCTGCA 1985

Qy 1801 AGTCAGATTCTGATATTTGAAAGATGTTAAATGTCGTCAGAAAGGGGACTTACACTGAGTTC 1860

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1986	Db		AGTCAGATTTCTGATATTTCAGAAAGATGGTAAAAATGGTGACAGAGGGGACTTACACTGAGTTTC	2045
1961	Qy	CTAAAACTCGGTATAGATATTTGGCTCCCTTTTAAAGAAAGGATTAATGAGGAAAGTGACAA	1920	
2046	Db	CTAAAACTCGGTATAGATATTTGGCTCCCTTTTAAAGAAAGGATTAATGAGGAAAGTGACAA	2105	
1921	Qy	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACTCTTCTCAGAGTCTTCGGTTTGG	1980	
2106	Db	CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACTCTTCTCAGAGTCTTCGGTTTGG	2165	
1981	Qy	TCTCAACAAATCTTCTAGACGCTCTTCAAGATGGTGCTCTGGAGAGCCAAAGATACAGAG	2040	
2166	Db	TCTCAACAAATCTTCTAGACGCTCTTCAAGATGGTGCTCTGGAGAGCCAAAGATACAGAG	2225	
2041	Qy	AATGTCACAGTTACACTATCAGAGGAGAACGGTCTCTGAAGGAAAGTTGGTTTCAGGCC	2100	
2226	Db	AATGTCACAGTTACACTATCAGAGGAGAACGGTCTCTGAAGGAAAGTTGGTTTCAGGCC	2285	
2101	Qy	TATAAGAAATTAATTCAGAGCTGGTGCTCACTGGGATTCCTTCAATTTCCCTATTCTCCTA	2160	
2286	Db	TATAAGAAATTAATTCAGAGCTGGTGCTCACTGGGATTCCTTCAATTTCCCTATTCTCCTA	2345	
2161	Qy	AACACTGCAGCTCAGGTTGCCTATGTGCTTTCAAGATTTGGTGCTTTCATACTGGGCAAAAC	2220	
2346	Db	AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTTGGTGCTTTCATACTGGGCAAAAC	2405	
2221	Qy	AAACAAAGTATGCTAAATGTCACTGTAATGGAGGAGGAAATGTAAACCGAGAGCTAGAT	2280	
2406	Db	AAACAAAGTATGCTAAATGTCACTGTAATGGAGGAGGAAATGTAAACCGAGAGCTAGAT	2465	
2281	Qy	CTTAACTGGTACTTAGGAAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340	
2466	Db	CTTAACTGGTACTTAGGAAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2525	
2341	Qy	GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACCTCTTCACAAACTTTTGCACAAAA	2400	
2526	Db	GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACCTCTTCACAAACTTTTGCACAAAA	2585	
2401	Qy	ATGTTTGAGTCAATCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCAATAGGNAGA	2460	
2586	Db	ATGTTTGAGTCAATCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCAATAGGNAAGA	2645	
2461	Qy	ATTTTAAATCGTTTCTCAAGACATTTGGACACTTGGATGATTTGCTGCGCTGACGTTT	2520	
2646	Db	ATTTTAAATCGTTTCTCAAGACATTTGGACACTTGGATGATTTGCTGCGCTGACGTTT	2705	
2521	Qy	TTAGATTTTCACAGACATTTGCTACAAAGTGTTGGTGCTCTCTGCGCTGGCCGCTG	2580	
2706	Db	TTAGATTTTCACAGACATTTGCTACAAAGTGTTGGTGCTCTCTGCGCTGGCCGCTG	2765	
2581	Qy	ATTCCTTGGATCGAAATACCTTGTTCCCTCTGGGAATCAATTTTCATTTTCTTCGGCGA	2640	
2766	Db	ATTCCTTGGATCGAAATACCTTGTTTCCCTCTGGGAATCAATTTTTCATTTTCTTCGGCGA	2825	
2641	Qy	TATTTTTTGGAAACGTCAGAGATGTGAAGCGCTGGAATCTACAACTCCGAGTCCAGTG	2700	
2826	Db	TATTTTTTGGAAACGTCAGAGATGTGAAGCGCTGGAATCTACAACTCCGAGTCCAGTG	2885	
2701	Qy	TTTTTCCCACTTGTCAATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2760	
2886	Db	TTTTTCCCACTTGTCAATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2945	
2761	Qy	GAGAGGTGTACAGGAACGTGTTTGTATGCAACAGATTTTACATTCAGAGGCTTGTTCTTG	2820	
2946	Db	GAGAGGTGTACAGGAACGTGTTTGTATGCAACAGATTTTACATTCAGAGGCTTGTTCTTG	3005	
2821	Qy	TTTTTTGACACGCTCCGCTGGTTCGCGCTGCTGGATGCCATCTGTGCCATGTTTGTCT	2880	
3006	Db	TTTTTTGACACGCTCCGCTGGTTCGCGCTGCTGGATGCCATCTGTGCCATGTTTGTCT	3065	
2881	Qy	ATCATCGTGTGCTTTGGGTCCCTGATTTCTGGCAAAAACTCTGGATGCGGGCAGGTTGGT	2940	

Db	3066	ATCATCGTTGCCCTTTGGGTCCCTGTATCTCTGGCAAAAACCTCTGGATGCCGGCAGGTTGGT	3120
Qy	2941	TTGGCACTGTCCTATGCGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTCTTCGACAAAGT	3000
Db	3126	TTGGCACTGTCCTATGCCCTCAGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT	3185
Qy	3001	GCTGAAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATTGAAATACACAGACCTTTGAA	3060
Db	3186	GCTGAAAGTTGAGAAATATGATGATCTCAGTAGAAAGGGTCAATTGAAATACACAGACCTTTGAA	3245
Qy	3061	AAAGAGCACCCTTTGGGAATATCAGAAACGCCACACCGAGCTGGGCCCATGAAGAGGTG	3120
Db	3246	AAAGAGCACCCTTTGGGAATATCAGAAACGCCACACCGAGCTGGGCCCATGAAGAGGTG	3305
Qy	3121	ATAATCTTTGACAAATGTGAACCTTCATGTACAGTTCAGGTGGGCCTCTGGTACTCTGAAGCAT	3180
Db	3306	ATAATCTTTGACAAATGTGAACCTTCATGTACAGTTCAGGTGGGCCTCTGGTACTCTGAAGCAT	3365
Qy	3181	CTGACAGCACTCAATTAATCACAAGAAAAAGTTGGCAATTTGTGGGAAGAACCCGAGCTGGGA	3240
Db	3366	CTGACAGCACTCAATTAATCACAAGAAAAAGTTGGCAATTTGTGGGAAGAACCCGAGCTGGGA	3425
Qy	3241	AAAAGTTCCTCACTCAGCCCTTTTAGATTTGTTCAGAACCCGAGTGAAGTAAAAATTTGGATT	3300
Db	3426	AAAAGTTCCTCACTCAGCCCTTTTAGATTTGTTCAGAACCCGAGTGAAGTAAAAATTTGGATT	3485
Qy	3301	GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAAAATGTCAATCATATA	3360
Db	3486	GATAAGATCTTGACAACTGAAATTTGGACTTCACGATTTAAGGAAGAAAAATGTCAATCATATA	3545
Qy	3361	CCTCAGGAAACCTGTTTTGTTTCACTCGGAAACAAATGAGGAAAAACCTGGATCCCTTTAATGAG	3420
Db	3546	CCTCAGGAAACCTGTTTTGTTTCACTCGGAAACAAATGAGGAAAAACCTGGATCCCTTTAATGAG	3605
Qy	3421	CACACGGATGAGGAACTGTGGAAATGCGTTTCAAGAGGTACAACTTAAAGAAACCATTGAA	3480
Db	3606	CACACGGATGAGGAACTGTGGAAATGCGTTTCAAGAGGTACAACTTAAAGAAACCATTGAA	3665
Qy	3481	GATCTTCCTGGTAAAAATGGATCTGAAATTAGCAGAAATCAGGATCCAAATTTTAGTGTGGGA	3540
Db	3666	GATCTTCCTGGTAAAAATGGATCTGAAATTAGCAGAAATCAGGATCCAAATTTTAGTGTGGGA	3725
Qy	3541	CAAGAGCAACTGGTGTGCCCTGCGGAGCAATTTCTCAGGAAAAATCAGATATTGATTATT	3600
Db	3726	CAAGAGCAACTGGTGTGCCCTGCGGAGCAATTTCTCAGGAAAAATCAGATATTGATTATT	3785
Qy	3601	GATGAAGCAGCGGCAAAATGTGGATCCAGAACTGATGAGTTAATACAAAAAAAATCCCG	3660
Db	3786	GATGAAGCAGCGGCAAAATGTGGATCCAGAACTGATGAGTTAATACAAAAAAAATCCCG	3844
Qy	3661	GAGAAATTTGCCCACTGCACCGTGCTAAACCATTTGCAACAGATTTGAACCACTATTATTGAC	3720
Db	3845	GAGAAATTTGCCCACTGCACCGTGCTAAACCATTTGCAACAGATTTGAACCACTATTATTGAC	3904
Qy	3721	AGCGCAAGAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT	3780
Db	3905	AGCGCAAGAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT	3964
Qy	3781	TTGCTGCAAAATAAAGAGAGCCCTATTTTTACAAGATGGTGCAACCTGGGCAAGGCGAGAA	3840
Db	3965	TTGCTGCAAAATAAAGAGAGCCCTATTTTTACAAGATGGTGCAACCTGGGCAAGGCGAGAA	4024
Qy	3841	GCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTAATCCACATATT	3900
Db	4025	GCGCTGCCCTCACTGAAACAGCAAAACAGGTATACCTTCAAAAGAAATTAATCCACATATT	4084
Qy	3901	GGTCACACTGCACCATGGTTACAAACACTTCCAAATGGAACGCGCCCTCGACCTTAACTATT	3960
Db	4085	GGTCACACTGCACCATGGTTACAAACACTTCCAAATGGAACGCGCCCTCGACCTTAACTATT	4144
Qy	3961	TTGAGACAGCACTGTGA 3978	
Db	4145	TTGAGACAGCACTGTGA 4162	



RESULT 12

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US-10-012-896-535
; Sequence 535, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuyu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-012-896-535

Query Match          99.7%; Score 3966; DB 13; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGCTGCCGTGTACACGAGGAGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 60
Db 186 ATGCTGCCGTGTACACGAGGAGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy 61 CGCGTGTTCTTCGTGGCTCAATCCCTTGTTHAAATTTGGCCATAAACGGAGATTAGAG 120
Db 246 CGCGTGTTCTTCGTGGCTCAATCCCTTGTTHAAATTTGGCCATAAACGGAGATTAGAG 305

Qy 121 GAAGATCATATGATTTCAGTGCTGCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG 180
Db 306 GAAGATCATATGATTTCAGTGCTGCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTG 365

Qy 181 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATCTTATTTTGGGAAATTTTACGTTA 240
Db 366 CAAGGGTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATCTTATTTTGGGAAATTTTACGTTA 425

Qy 241 ACAAGCAATCATAAAGTGTACTGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 300
Db 426 ACAAGCAATCATAAAGTGTACTGAAATCTTATTTAGTTTGGGAAATTTTACGTTA 485

Qy 301 ATTGAGAAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAATTTTATTAATTTT 360
Db 486 ATTGAGAAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAATTTTATTAATTTT 545

Qy 361 GAAAAATTATGATCCCATGGATTCTGTGGCTTTTGAACACAGCGTACGCTATGCCACGGTG 420

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Db 546 GAAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCATATGCCACGGTG 605
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Db 606 CTGACTTTTTTGCAGCGCTCATTTTGGCTATCTACTGTCATCACTATATTTTATCAGTTTCAG 665
Qy 481 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGCGACTTCGT 540
Db 666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGCGACTTCGT 725
Qy 541 CTTAGTAACATGCGCCATGCGGAGAACAAACACAGCCAGATAGTCAATCTCTGTCTCAAT 600
Db 726 CTTAGTAACATGCGCCATGCGGAGAACAAACACAGCCAGATAGTCAATCTCTGTCTCAAT 785
Qy 601 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCCTGTGGGAGGACCACTG 660
Db 786 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCCTGTGGGAGGACCACTG 845
Qy 661 CAGCGCATCGCAGTACTGCCCTACTCTGGATGAGATAGGAATATCGTGCCTTGTCTGG 720
Db 846 CAGCGCATCGCAGTACTGCCCTACTCTGGATGAGATAGGAATATCGTGCCTTGTCTGG 905
Qy 721 ATGCGACTTCTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTTGTTCTCATCA 780
Db 906 ATGCGACTTCTAATCATTTCTCTGCCCTTGCAGAGCTGTTTGGGAAGTTGTTCTCATCA 965
Qy 781 CTGAGGAGTAAACTGCAACTTTTACCGATGCCAGGATCAGGACCATCAATGAAGTTATA 840
Db 966 CTGAGGAGTAAACTGCAACTTTTACCGATGCCAGGATCAGGACCATCAATGAAGTTATA 1025
Qy 841 ACTGGTATAAGGATAATAAAAAATGTCAGCCCTGGGAAAAAGTCATTTCAAATCTTATACC 900
Db 1026 ACTGGTATAAGGATAATAAAAAATGTCAGCCCTGGGAAAAAGTCATTTCAAATCTTATACC 1085
Qy 901 AATTTGAGAAAGAGGAGATTTCAGAGATTCTGAGAAAGTTCTCTCCCTCAGGGGATGAAT 960
Db 1086 AATTTGAGAAAGAGGAGATTTCAGAGATTCTGAGAAAGTTCTCTCCCTCAGGGGATGAAT 1145
Qy 961 TTGGCTTCGTTTTCAGTGAAGCAAAATCATCGTGTCTGTGACCTTCACCACTACGCTG 1020
Db 1146 TTGGCTTCGTTTTCAGTGAAGCAAAATCATCGTGTCTGTGACCTTCACCACTACGCTG 1205
Qy 1021 CTCTCGGCAAGTGTATCACAGCCGCGGTGTTCTGTGGCAGTGAGCGTGTATGGGGCT 1080
Db 1206 CTCTCGGCAAGTGTATCACAGCCGCGGTGTTCTGTGGCAGTGAGCGTGTATGGGGCT 1265
Qy 1081 GTGCGGCTGACGGTTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTTCAGAGGCAATC 1140
Db 1266 GTGCGGCTGACGGTTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTTCAGAGGCAATC 1325
Qy 1141 GTCAGCATCCGAGAAATCCAGACCTTTTGTCTACTTGTATGATGATATCACAGCGCAACCGT 1200
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Qy 1201 CAGCTGCCGTGAGATGGTAAAGAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGAT 1260
Db 1386 CAGCTGCCGTGAGATGGTAAAGAGATGGTGCATGTGCAGGATTTTACTGCTTTTGGAT 1445
Qy 1261 AAGGCATCAGAGACCCCACTCTCAAGGCGCTTCTTTTACTGTCTGAGACCTTGGGCAATTG 1320
Db 1446 AAGGCATCAGAGACCCCACTCTCAAGGCGCTTCTTTTACTGTCTGAGACCTTGGGCAATTG 1505
Qy 1321 TTAGCTGTGTGCGGCGGCGGAGCGGAGATCATCACTGTCTAGTTCGCTGCTCGG 1380
Db 1506 TTAGCTGTGTGCGGCGGCGGAGCGGAGATCATCACTGTCTAGTTCGCTGCTCGG 1565
Qy 1381 GAATTGGCCCAAGTCAACGGGCTGGTTCAGCGTGCATGGAAGAAATTCCTATGCTCTCAG 1440
Db 1566 GAATTGGCCCAAGTCAACGGGCTGGTTCAGCGTGCATGGAAGAAATTCCTATGCTCTCAG 1625
Qy 1441 CAGCCCTTGGGTGTTCTCGGGAACCTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500

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Db 1626 CAGCCCTGGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTTGGGAAGAAATACGAA 1685  
Qy 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTTG 1560  
Db 1686 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTTG 1745  
Qy 1561 GAGGATGCTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGSCAGAAA 1620  
Db 1746 GAGGATGCTGATCTGACTGTGATAGGAGATCGGGGAACCAAGCTGAGTGGAGGSCAGAAA 1805  
Qy 1621 GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGGACGAT 1680  
Db 1806 GCAGGGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGGACGAT 1865  
Qy 1681 CCTCTAGTGCAGTAGATGCGGAAGTTAGCAGACACATTTGTTGCAATCTGTGTATTTGTCAA 1740  
Db 1866 CCTCTAGTGCAGTAGATGCGGAAGTTAGCAGACACATTTGTTGCAATCTGTGTATTTGTCAA 1925  
Qy 1741 ATTTTGCATGAGAAGATCACAAATTTTGTAGTGACTCATCAGTTGTCAGTACCTCAAGCTGCA 1800  
Db 1926 ATTTTGCATGAGAAGATCACAAATTTTGTAGTGACTCATCAGTTGTCAGTACCTCAAGCTGCA 1985  
Qy 1801 AGTCAGATTCGTATATTTCAAGATGTGTAAATGTGTCAGAGGGGACTTACACTGAGTTC 1860  
Db 1986 AGTCAGATTCGTATATTTCAAGATGTGTAAATGTGTCAGAGGGGACTTACACTGAGTTC 2045  
Qy 1861 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATGAGGAAGTGAACAA 1920  
Db 2046 CTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATGAGGAAGTGAACAA 2105  
Qy 1921 CCTCCAGTCCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980  
Db 2106 CCTCCAGTCCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165  
Qy 1981 TCTCAACAAATCTCTAGACCTCTCTGAAAGATGGTCTCTGAGAGCCCAAGATACAGAG 2040  
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Qy 2041 AATGTCCTCAGTTACACTATCAGAGGAGAACCGTTCTGAAAGAAAGTTGGTTTCAGGCC 2100  
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Qy 2101 TATAAGAAATTAATTCAGAGCTGGTGCTCACTGGAATGCTCTCATTTTCCATTATTCCTTA 2160  
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Qy 2161 AACACTGCAGCTCAGGTGCTATGTCTTCAAGATTTGGTGGCTTTTCATACTGGGCAAC 2220  
Db 2346 AACACTGCAGCTCAGGTGCTATGTCTTCAAGATTTGGTGGCTTTTCATACTGGGCAAC 2405  
Qy 2221 AACAAAGTATGCTAAATGTACATGTAATGGAGGAGGAATGTAACCGAGAGCTAGAT 2280  
Db 2406 AACAAAGTATGCTAAATGTACATGTAATGGAGGAGGAATGTAACCGAGAGCTAGAT 2465  
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Qy 2341 GCAAGATCTCTATTTGGTATTTCTAGCTCCTTGTAACTCTTTCACAAACTTTGCAACAAA 2400  
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Qy 2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTCACGTTT 2520  
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Qy 2521 TTAGATTTTCATCCAGACATTTGCTACAAAGTGGTGGTGGTCTCTGTGGCTGTGGCCGTG 2580  
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Qy 2581 ATTCTTTGGATCGCAATACCCCTTTGGTTCCCTTTGGATCATTTTTCATTTTCTTCGSCGA 2640  
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Qy 2641 TATTTTGTGAAACGTCAGAGATGTGAAGCGCTTGAAATCTACAACTCGAGGTCCAGTG 2700  
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Qy 2701 TTTTCCACATTTGTCACTTTCTCTCAGGGGCTCTGGAACCATCCGGGCATATCAAGACGAA 2760  
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Qy 2761 GAGAGGTGTCAGAACTGTGTTTGTATGACACACAGGATTTACATTCAGAGGCTTGGTTCTTG 2820  
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Db 3126 TTGGCACTGCTTATGCCCTCAGCTCATCGGGGATGTTTTCAGTGGTGTGTTGCACAAGT 3185  
Qy 3001 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAGGGTCAATGAATACACAGAGCTTTGAA 3060  
Db 3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAGGGTCAATGAATACACAGAGCTTTGAA 3245  
Qy 3061 AAGAAGACCTTTGGGAATATCAGAAACGCCACCACTGGCTGGCCCCCATGGAAGAGTG 3120  
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Qy 3481 GATCTTCTGTAATAATGGAATGATTAATAGCAGAAATCAGATCCAAATTTTAGTGTGGA 3540  
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Qy 3601 GATGAAGCGACGGCAAAATGTGGATCCAAAGATCTGATGAGTTAATACAAAAAATCCGG 3660  
Db 3786 GATGAAGCGACGGCAAAATGTGGATCCAAAGATCTGATGAGTTAATACAAAAAATCCGG 3844

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Db 3845 GAGAAATTTGCCACTGCACCGTCTAAACCAATTGCACACAGATTGAACACCAATTATTGAC 3904
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QY 3901 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGACAGCCCTCGACCTTAACATT 3960
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QY 3961 TTCGAGACAGCACTGTGA 3978
Db 4145 TTCGAGACAGCACTGTGA 4162

RESULT 13
US-10-010-940-535
; Sequence 535, Application US/10010940
; Publication No. US20030088062A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010,940
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-940-535

Query Match 99.7%; Score 3966; DB 14; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGCTGCCCGTGTACAGGAGGTGAAGCCCAACCGCTGCGAGGACGGAACCTCTGTCTCA 60
Db 186 ATGCTGCCCGTGTACAGGAGGTGAAGCCCAACCGCTGCGAGGACGGAACCTCTGTCTCA 245
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Db 246 CGCGTGTCTTCTGCTGCTCAATCCCTGTTTAAATTGGCCATAAAGCGAGATTAGAG 305
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Db 306 GAAGATGATATGATTTCAGTGTCTGCCAAGAACCGCTCAGACACCTTTGGAGAGAGTTG 365
QY 181 CAAGGGTTCTGGGATAAAGAGTTTAAAGACTGAGATGACGACAGAACCTTCTTTTA 240
Db 366 CAAGGGTTCTGGGATAAAGAGTTTAAAGACTGAGATGACGACAGAACCTTCTTTTA 425
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QY 241 ACAAGAGCAATCATAAAGTGTACTTGAAATCTTATTAGTTTGGGAATTTTACGTGA 300
Db 426 ACAAGAGCAATCATAAAGTGTACTTGAAATCTTATTAGTTTGGGAATTTTACGTGA 485
QY 301 ATTGAGGAAAGTGCACAAAGTAATTCAGCCCAATATTTTGGGAAATAATTATTAATTTT 360
Db 486 ATTGAGGAAAGTGCACAAAGTAATTCAGCCCAATATTTTGGGAAATAATTATTAATTTT 545
QY 361 GAAATATTATGATCCCATGATTTCTGTGGCTTTGAAACACAGCGTAGCCCTATGCCACGGTG 420
Db 546 GAAATATTATGATCCCATGATTTCTGTGGCTTTGAAACACAGCGTAGCCCTATGCCACGGTG 605
QY 421 CTGACTTTTTTGCACGCTCATTTTGGCTATATCTGCACTCACTTATATTTTATCAGCTTCAG 480
Db 606 CTGACTTTTTTGCACGCTCATTTTGGCTATATCTGCACTCACTTATATTTTATCAGCTTCAG 665
QY 481 TGTGCTGGGATGAGGTTTACGATAGCCATGTGCGCATATGATTTATCGGAAGCACTTCGT 540
Db 666 TGTGCTGGGATGAGGTTTACGATAGCCATGTGCGCATATGATTTATCGGAAGCACTTCGT 725
QY 541 CTTAGTAACATGGCCATGGGGAAGACCAACACAGSCCAGATAGTCAATCTGCTGCCAAT 600
Db 726 CTTAGTAACATGGCCATGGGGAAGACCAACACAGSCCAGATAGTCAATCTGCTGCCAAT 785
QY 601 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCGAGGACCACTG 660
Db 786 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGCGAGGACCACTG 845
QY 661 CAGCGGATCGCAGTGACTGCGCTACTCTGGAATGAGATAGGAATATCTGCTTCTGCTGGG 720
Db 846 CAGCGGATCGCAGTGACTGCGCTACTCTGGAATGAGATAGGAATATCTGCTTCTGCTGGG 905
QY 721 ATGCGAGTTCTAAATCATTCTCTGCCCTTCGCAAGCTGTTTGGGAAGTTGTTCTCATCA 780
Db 906 ATGCGAGTTCTAAATCATTCTCTGCCCTTCGCAAGCTGTTTGGGAAGTTGTTCTCATCA 965
QY 781 CTGAGGAGTAAAACTGCAACTTTTCAAGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840
Db 966 CTGAGGAGTAAAACTGCAACTTTTCAAGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025
QY 841 ACTGTTATAGGATAAATAAATGTAGCCTGGGAAAGTCAATTTTCAATCTTATTACC 900
Db 1026 ACTGTTATAGGATAAATAAATGTAGCCTGGGAAAGTCAATTTTCAATCTTATTACC 1085
QY 901 AATTTGAGAAAGAGGAGATTTCAGATTTCTGAGAGTTTCTGCTCAGGGGATGAAT 960
Db 1086 AATTTGAGAAAGAGGAGATTTCAGATTTCTGAGAGTTTCTGCTCAGGGGATGAAT 1145
QY 961 TTGGCTTCTGTTTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCACCACTTACCGTG 1020
Db 1146 TTGGCTTCTGTTTTTTCAGTGAAGCAAAATCATCTGTTTGTGACCTTCACCACTTACCGTG 1205
QY 1021 CTCCTCGGCAAGTGTGATCAGACGAGCGCGGTGTTCTGTCAGTGAAGCTGTATGGGCT 1080
Db 1206 CTCCTCGGCAAGTGTGATCAGACGAGCGCGGTGTTCTGTCAGTGAAGCTGTATGGGCT 1265
QY 1081 GTGCGGCTGACGGTTACCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGCAATC 1140
Db 1266 GTGCGGCTGACGGTTACCTTCTTCCCTCAGCCATTGAGAGGGTGTGAGAGCAATC 1325
QY 1141 GTCAGCATCCGAAGAAATCCAGACCTTTTGTCTACTTGTATGATATATCAGCGCAACCGT 1200
Db 1326 GTCAGCATCCGAAGAAATCCAGACCTTTTGTCTACTTGTATGATATATCAGCGCAACCGT 1385
QY 1201 CAGCTGCCGTGAGATGTTAAAGATGGTGCATGTGAGGATTTTATCTGCTTTTGGGAT 1260
Db 1386 CAGCTGCCGTGAGATGTTAAAGATGGTGCATGTGAGGATTTTATCTGCTTTTGGGAT 1445
QY 1261 AAGCATCAGAGACCCCACTCTACAGGCTTTCTTTACTGTACAGACCTGGGGAATTG 1320
Db 1446 AAGCATCAGAGACCCCACTCTACAGGCTTTCTTTACTGTACAGACCTGGGGAATTG 1505
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QY	1321	TTAGCTGTGGTCCGCCGCGGAGCAGGGAAGTCATCACTGTTTAAGTCGCGTCTCGG	1380
Db	1506	TTAGCTGTGGTCCGCCGCGGAGCAGGGAAGTCATCACTGTTTAAGTCGCGTCTCGG	1565
QY	1381	GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAAATGCTATGTCTCAG	1440
Db	1566	GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAAATGCTATGTCTCAG	1625
QY	1441	CAGCCCTGGGTGTTCTCGGGAACCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA	1500
Db	1626	CAGCCCTGGGTGTTCTCGGGAACCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA	1685
QY	1501	AAGGAACGATATGAAAAGTCATAAAGCTTTGTCTCTGTAAGAAAGGATTTACAGCTGTG	1560
Db	1686	AAGGAACGATATGAAAAGTCATAAAGCTTTGTCTCTGTAAGAAAGGATTTACAGCTGTG	1745
QY	1561	GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCCAGCTGAGTGAGGGGCAGAAA	1620
Db	1746	GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCCAGCTGAGTGAGGGGCAGAAA	1805
QY	1621	GCACGGGTAAACCTTGCAGAGCAGTGATCAAGATGCTGACATCTATCTCTCGGACGAT	1680
Db	1806	GCACGGGTAAACCTTGCAGAGCAGTGATCAAGATGCTGACATCTATCTCTCGGACGAT	1865
QY	1681	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTTGTTCCGAACCTGTGATTTGTCAA	1740
Db	1866	CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTTGTTCCGAACCTGTGATTTGTCAA	1925
QY	1741	ATTTTGCATGAGAAAGATCACAAATTTTAGTGACTCATCAGTTGCACTACCTCAAAGCTGCA	1800
Db	1926	ATTTTGCATGAGAAAGATCACAAATTTTAGTGACTCATCAGTTGCACTACCTCAAAGCTGCA	1985
QY	1801	AGTCAGATTTCTGATTTAAAGATGGTAAATGTGTGCAGAGGGGACTTACACTGAGTTC	1860
Db	1986	AGTCAGATTTCTGATTTAAAGATGGTAAATGTGTGCAGAGGGGACTTACACTGAGTTC	2045
QY	1861	CTAAATCTGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGGAAAGTGAACAA	1920
Db	2046	CTAAATCTGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATATAGGAAAGTGAACAA	2105
QY	1921	CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTTCTCAGAGTCTTCGGTTGG	1980
Db	2106	CCTCCAGTTCAGGAACCTCCACACTAAGGAATCGTACCTTTCTCAGAGTCTTCGGTTGG	2165
QY	1981	TCTCAACAAATCTTACAGCCCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAG	2040
Db	2166	TCTCAACAAATCTTACAGCCCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAG	2225
QY	2041	AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC	2100
Db	2226	AATGTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC	2285
QY	2101	TATAAGAAATTAATTCAGAGCTGGTGTCTCAGTGAATGTCTTCAATTTCTTTATCTCCTA	2160
Db	2286	TATAAGAAATTAATTCAGAGCTGGTGTCTCAGTGAATGTCTTCAATTTCTTTATCTCCTA	2345
QY	2161	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTTCACTGGGGAAC	2220
Db	2346	AACACTGCAGCTCAGGTTGCTATGTGCTTCAAGATTTGGTGGCTTTTCACTGGGGAAC	2405
QY	2221	AAACAAAGATATGCTAAATGTCACTGTAATGAGGAGGAATGTAAACCGAGAAGCTAGAT	2280
Db	2406	AAACAAAGATATGCTAAATGTCACTGTAATGAGGAGGAATGTAAACCGAGAAGCTAGAT	2465
QY	2281	CTTAACCTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2340
Db	2466	CTTAACCTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATA	2525
QY	2341	GCAAGATCTCTATTGGTATTCTAGCTCTCTGTTAACTTCACTTCAACAACTTTGCAACAAA	2400
Db	2526	GCAAGATCTCTATTGGTATTCTAGCTCTCTGTTAACTTCACTTCAACAACTTTGCAACAAA	2585
QY	2401	ATGTTTGAGTCAATTTCTGAAGCTCCGCTATTAATTTCTTTGATAGAAATCCAATAGGAAGA	2460

Db	2586	ATGTTTGAGTCAATTTCTGAAGCTCCGCTATTATTTCTTTGATAGAAATCCAATAGGAAGA	2645
QY	2461	ATTTTAAATCGTTTCTCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACGCTTT	2520
Db	2646	ATTTTAAATCGTTTCTCAAAGACATTTGGACACTTTGGATGATTTGCTGCGCTGACGCTTT	2705
QY	2521	TTAGATTTTCATCAGACATTTGCTACAGTGGTGGTGGTCTCTGTTGGCTGTGCGCGTG	2580
Db	2706	TTAGATTTTCATCAGACATTTGCTACAGTGGTGGTGGTCTCTGTTGGCTGTGCGCGTG	2765
QY	2581	ATTCTTTGGATCGCAATACCTTTGGTTCCCTTTGGAAATCAATTTTCTTTCTCGGCGA	2640
Db	2766	ATTCTTTGGATCGCAATACCTTTGGTTCCCTTTGGAAATCAATTTTCTTTCTCGGCGA	2825
QY	2641	TATTTTGTGAAACGCTCAAGAGATGTGAAGCGCTTGAATCTACAACTCGGAGTCCAGTG	2700
Db	2826	TATTTTGTGAAACGCTCAAGAGATGTGAAGCGCTTGAATCTACAACTCGGAGTCCAGTG	2885
QY	2701	TTTTCACACTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2760
Db	2886	TTTTCACACTGTCTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA	2945
QY	2761	GAGAGGTGTGAGGAACTGTGTTGATGCACACAGGATTTTACATTCAGAGGCTTGGTTCTTG	2820
Db	2946	GAGAGGTGTGAGGAACTGTGTTGATGCACACAGGATTTTACATTCAGAGGCTTGGTTCTTG	3005
QY	2821	TTTTTGACAAAGCTCCGCTGGTTCGCGCTCGCTCTGATGCCATCTGTGCCATGTTTGTGTC	2880
Db	3006	TTTTTGACAAAGCTCCGCTGGTTCGCGCTCGCTCTGATGCCATCTGTGCCATGTTTGTGTC	3065
QY	2881	ATCATCGTTCCTTTGGGTCCCTGATTTCTGCGCAAAACTCTGGATGCCGGCAGGTTGGT	2940
Db	3066	ATCATCGTTCCTTTGGGTCCCTGATTTCTGCGCAAAACTCTGGATGCCGGCAGGTTGGT	3125
QY	2941	TTGGCACTGTCTATGCCCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3000
Db	3126	TTGGCACTGTCTATGCCCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT	3185
QY	3001	GCTGAAGTTCAGAAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACTTGAA	3060
Db	3186	GCTGAAGTTCAGAAATATGATGATCTCAGTAGAAGGGTCAATTGAATACACAGACTTGAA	3245
QY	3061	AAAGACACCTTTGGGAATATCAGAACGCCACACAGCTCGGCCCATGAAGGAGTG	3120
Db	3246	AAAGACACCTTTGGGAATATCAGAACGCCACACAGCTCGGCCCATGAAGGAGTG	3305
QY	3121	ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT	3180
Db	3306	ATAATCTTTGACAAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCAT	3365
QY	3181	CTGACAGCATCTAATTAATCAGAAAGAGTTGGCATTTGGGAAGAACCCGGAGCTGGA	3240
Db	3366	CTGACAGCATCTAATTAATCAGAAAGAGTTGGCATTTGGGAAGAACCCGGAGCTGGA	3425
QY	3241	AAAAGTTCCTCATCTCAGCCCTTTTAGATTGTTCAGAACCCGAGGTAATAATTTGGATT	3300
Db	3426	AAAAGTTCCTCATCTCAGCCCTTTTAGATTGTTCAGAACCCGAGGTAATAATTTGGATT	3485
QY	3301	GATAAGATCTTGACAACTGAAATTTGGAATTCACCGATTTAAGGAAGAAAAATGCTCAATCATA	3360
Db	3486	GATAAGATCTTGACAACTGAAATTTGGAATTCACCGATTTAAGGAAGAAAAATGCTCAATCATA	3545
QY	3361	CCTCAGGAACTGTGTTTGTTCATCTGGAACTATGAGGAAAAACCTGGATCCCTTTAATGAG	3420
Db	3546	CCTCAGGAACTGTGTTTGTTCATCTGGAACTATGAGGAAAAACCTGGATCCCTTTAATGAG	3605
QY	3421	CACACGATGAGGAACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA	3480
Db	3606	CACACGATGAGGAACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCAATTGAA	3665
QY	3481	GATCTTCTGGTAAAAATGGATACCTGAATATGACAGAAATCAGGAATCCAATTTAGTTGGTA	3540

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Qy 3541 CAAGACAACTGGTGTGCTTCCAGGCGCAATCTCAGAGAAAATCAGATATGATTAAT 3600  
Db 3726 CAAGACAACTGGTGTGCTTCCAGGCGCAATCTCAGAGAAAATCAGATATGATTAAT 3785  
Qy 3601 GATGAAGCGGCGCAAAATGTGGATCCAGAACTGATGATTTAAATACAAAAAATCCGG 3660  
Db 3786 GATGAAGCGGCGCAAAATGTGGATCCAGAACTGATGATTTAAATACAAAAAATCCGG 3844  
Qy 3661 GAGAAATTTGCCCACTGACCGCTGCTAACCAATTCGACATTCGACATTTGATGAC 3720  
Db 3845 GAGAAATTTGCCCACTGACCGCTGCTAACCAATTCGACATTTGATGAC 3904  
Qy 3721 AGCGACAGATTAATGCTTTTAGATTTAGAGGAGCTGAAAGAAATATGATGACCGCTATGTT 3780  
Db 3905 AGCGACAGATTAATGCTTTTAGATTTAGAGGAGCTGAAAGAAATATGATGACCGCTATGTT 3964  
Qy 3781 TTGCTGCAAAATAAGAGAGCTTAATTTTAAAGATGTGCAAACTGGGCAAGGCGAA 3840  
Db 3965 TTGCTGCAAAATAAGAGAGCTTAATTTTAAAGATGTGCAAACTGGGCAAGGCGAA 4024  
Qy 3841 GCGCTGCCCTCACTGAAAGCAAGCAAGCAAGTATCTTCAAAAGAAATTTATCCACATAT 3900  
Db 4025 GCGCTGCCCTCACTGAAAGCAAGCAAGCAAGTATCTTCAAAAGAAATTTATCCACATAT 4084  
Qy 3901 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 3960  
Db 4085 GGTCACTGACCACTGGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACTATT 4144  
Qy 3961 TTCGAGACAGCACTGTGA 3978  
Db 4145 TTCGAGACAGCACTGTGA 4162

## RESULT 14

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; Sequence 535, Application US/10144678A  
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; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Vinals y de Bassols, Carlota  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Deng, Ta  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C28  
; CURRENT APPLICATION NUMBER: US/10/144.678A  
; CURRENT FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 1033  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 535  
; LENGTH: 6082

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-144-678A-535

## Query Match

Best Local Similarity 99.7%; Score 3966; DB 16; Length 6082;  
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGCTGCCCTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGGAACTCTCTGCTCA 60  
Db 186 ATGCTGCCCTGTACAGGAGGTGAAGCCCAACCCGCTGCAGGACGGAACTCTCTGCTCA 245  
Qy 61 CGCGTGTCTTCTGTGGTCAATCCCTGTGTTAAATTTGGCCATAAAGAGATAGAG 120  
Db 246 CGCGTGTCTTCTGTGGTCAATCCCTGTGTTAAATTTGGCCATAAAGAGATAGAG 305  
Qy 121 GAAGATCATATGATTTTCAAGTGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGGTTG 180  
Db 306 GAAGATCATATGATTTTCAAGTGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGGTTG 365  
Qy 181 CAAGGGTCTTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGCTTCTTTA 240  
Db 366 CAAGGGTCTTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGCTTCTTTA 425  
Qy 241 ACAAGACCAATCAATAAGTGTACTGGAATCTTATTTAGTTTGGAAATTTTACGTTA 300  
Db 426 ACAAGACCAATCAATAAGTGTACTGGAATCTTATTTAGTTTGGAAATTTTACGTTA 485  
Qy 301 ATTGAGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTTATTTT 360  
Db 486 ATTGAGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTTATTTT 545  
Qy 361 GAAAAATATGATCCCATGGAATCTGTGGCTTTTGAACACAGCTATGCCACGCTG 420  
Db 546 GAAAAATATGATCCCATGGAATCTGTGGCTTTTGAACACAGCTATGCCACGCTG 605  
Qy 421 CTGACTTTTTGACGCTCATTTTGGCTATATCTGCATCACTATATTTTATCACGTTTCA 480  
Db 606 CTGACTTTTTGACGCTCATTTTGGCTATATCTGCATCACTATATTTTATCACGTTTCA 665  
Qy 481 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACTTCGT 540  
Db 666 TGTGCTGGGATGAGTTTACGAGTAGCCATGTGCCATATGATTTATCGAAGGCACTTCGT 725  
Qy 541 CTTAGTAAACATGCGCATGCGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCAAT 600  
Db 726 CTTAGTAAACATGCGCATGCGGGAAGACAAACACAGGCCAGATAGTCAATCTGCTGCAAT 785  
Qy 601 GATGTGAACAAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGCTGGGAGGACCACTG 660  
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Db 966 CTGAGGAGTAAAACTGCAACTTTTACGAGTCCAGGATCAGGACCATGAATGAAGTTATA 1025  
Qy 841 ACTGGTATAAGGATAATAAAAAATGATCGCTGGGAAAAAGTCATTTTCAAAATCTTATTACC 900  
Db 1026 ACTGGTATAAGGATAATAAAAAATGATCGCTGGGAAAAAGTCATTTTCAAAATCTTATTACC 1085  
Qy 901 AATTTCGAGAAAGAGGATTTTCCAGATTTCTGAGAGTTCTGCTCCCTCAGGGGATGAAT 960  
Db 1086 AATTTCGAGAAAGAGGATTTTCCAGATTTCTGAGAGTTCTGCTCCCTCAGGGGATGAAT 1145  
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Db 1146 |||||TTGGCTTGGTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTCCACCTACGTG 1205  
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Qy 1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
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Qy 1741 ATTTTGCATGAGAGATCACAAATTTTATGATCATCAGTTGTCAGTACCTCAAAAGCTGCA 1800  
Db 1926 ATTTTGCATGAGAGATCACAAATTTTATGATCATCAGTTGTCAGTACCTCAAAAGCTGCA 1985  
Qy 1801 AGTCAGATTTCTGATATTTGAAGATGTTAAATGTGTGAGAGGGGACTTACACTGAGTTC 1860  
Db 1986 AGTCAGATTTCTGATATTTGAAGATGTTAAATGTGTGAGAGGGGACTTACACTGAGTTC 2045  
Qy 1861 CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA 1920  
Db 2046 CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACAA 2105  
Qy 1921 CCTCCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980  
Db 2106 CCTCCAGTTCAGGAATCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165  
Qy 1981 TCTCAAAATCTTAGACCTCTTGAAGATGGTCTCTGAGAGGCCAAGATACAGAG 2040  
Db 2166 TCTCAAAATCTTAGACCTCTTGAAGATGGTCTCTGAGAGGCCAAGATACAGAG 2225  
Qy 2041 AATGTCCAGTTACACTATCAGAGGAAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCC 2100

Db 2226 AATGTCCAGTTACACTATCAGAGGAAACCGTTCTGAAGAAAGTTGGTTTTCAGGCC 2285  
Qy 2101 TATAAGAAATTTACTTTACAGAGCTGGTGTCTCACTGATTTGTCTTCAATTTTCCCTATTTCTCCTA 2160  
Db 2286 TATAAGAAATTTACTTTACAGAGCTGGTGTCTCACTGATTTGTCTTCAATTTTCCCTATTTCTCCTA 2345  
Qy 2161 AACACTGCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTTCATACTGGGCAAAAC 2220  
Db 2346 AACACTGCAGCTCAGGTTGCTATGTCTTCAAGATTTGGTGGCTTTTCATACTGGGCAAAAC 2405  
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Qy 2281 CTTAACTGGTACTTTAGGAATTTAATCAGGTTTAACTGTAGCTACCGTCTCTTTTGGGATA 2340  
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Qy 2881 ATCATCGTTCCTTTTGGTCCCTGATTTCTGCAAAAACTCTGGATGCGGCGAGTGGT 2940  
Db 3066 ATCATCGTTCCTTTTGGTCCCTGATTTCTGCAAAAACTCTGGATGCGGCGAGTGGT 3125  
Qy 2941 TTGGCACTGCTTATGCCCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3000  
Db 3126 TTGGCACTGCTTATGCCCCCTCAGCTCATGGGATGTTTTCAGTGGTGTGTTTCGACAAAGT 3185  
Qy 3001 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGCTCAATGAAATACACAGACTTGAA 3060  
Db 3186 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGCTCAATGAAATACACAGACTTGAA 3245  
Qy 3061 AAAGAACCTTTGGGAATATCAGAAACGCCACACAGCTCGGCCCAATGAAGGAGTG 3120  
Db 3246 AAAGAACCTTTGGGAATATCAGAAACGCCACACAGCTCGGCCCAATGAAGGAGTG 3305  
Qy 3121 ATAATCTTTGACAAATGTGAACCTTCATGTAAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3180  
Db 3306 ATAATCTTTGACAAATGTGAACCTTCATGTAAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3365

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Qy 3181 CTGACAGCACTCATTAATCAAGAAAGGTTGGCAATGTTGGAAAGAACCGGAGCTGGA 3240
Db 3366 CTGACAGCACTCATTAATCAAGAAAGGTTGGCAATGTTGGAAAGAACCGGAGCTGGA 3425
Qy 3241 AAAAGTTCCCTCATCTAGCCCTTTTAGATGTGCAGAACCCGGAAGGTAAATTTGGATT 3300
Db 3426 AAAAGTTCCCTCATCTAGCCCTTTTAGATGTGCAGAACCCGGAAGGTAAATTTGGATT 3485
Qy 3301 GATAAGATCTTGACAACCTGGAATTTGACCTTCAAGATTTAAGGAAGAAATGTCATCATATA 3360
Db 3486 GATAAGATCTTGACAACCTGGAATTTGACCTTCAAGATTTAAGGAAGAAATGTCATCATATA 3545
Qy 3361 CCTCAGGAACCTGTTTGTTCACCTGGAAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3420
Db 3546 CCTCAGGAACCTGTTTGTTCACCTGGAAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605
Qy 3421 CACAGGATGAGGAACCTGTGAATGCTTACAGAGGTACAACTTAAGAAACCAATTGAA 3480
Db 3606 CACAGGATGAGGAACCTGTGAATGCTTACAGAGGTACAACTTAAGAAACCAATTGAA 3665
Qy 3481 GATCTTCTGTAAATGGAATGACTGAATTTAGCAGAACTCAGGATCCAAATTTTAGTGTGGA 3540
Db 3666 GATCTTCTGTAAATGGAATGACTGAATTTAGCAGAACTCAGGATCCAAATTTTAGTGTGGA 3725
Qy 3541 CAAAGACAACCTGGTGTGCTTTCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT 3600
Db 3726 CAAAGACAACCTGGTGTGCTTTCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT 3785
Qy 3601 GATGAAGGACGGCAATGTGGATGCTCAAGAACTGATGATGTTAATACAAAAAATCCGG 3660
Db 3786 GATGAAGGACGGCAATGTGGATGCTCAAGAACTGATGATGTTAATACAAAAAATCCGG 3844
Qy 3661 GAGAAATTTGCCCACTGACCGCTCAACCAATTCACACAGATTTGAACCACTATTATGAC 3720
Db 3845 GAGAAATTTGCCCACTGACCGCTCAACCAATTCACACAGATTTGAACCACTATTATGAC 3904
Qy 3721 AGGCACAAGATAATGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3780
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Qy 3781 TTGCTGCAAAATAAGAGAGCTATTTTAAAGATGTGCAACAACTGGGCAAGCGAGAA 3840
Db 3965 TTGCTGCAAAATAAGAGAGCTATTTTAAAGATGTGCAACAACTGGGCAAGCGAGAA 4024
Qy 3841 GCGCTGCCCTCACTGAACAGCAAAACAGTATACCTTCAAAAGAAATTTATCCACATATT 3900
Db 4025 GCGCTGCCCTCACTGAACAGCAAAACAGTATACCTTCAAAAGAAATTTATCCACATATT 4084
Qy 3901 GGTCACTGACCACTGGTTTACAAACACTTCCCAATGGACAGCCCTCGACCTTAACCTATT 3960
Db 4085 GGTCACTGACCACTGGTTTACAAACACTTCCCAATGGACAGCCCTCGACCTTAACCTATT 4144
Qy 3961 TTCGAGACAGCACTGTGA 3978
Db 4145 TTCGAGACAGCACTGTGA 4162

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RESULT 15
US-10-294-025-535
; Sequence 535, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: Fast-Seq for Windows Version 3.0

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; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-535

Query Match      99.7%; Score 3966; DB 16; Length 6082;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3977; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 186 ATGCTGCCGTGTACACGAGGTGAAGCCCAACCGCTGCAGGAGCGGAACCTCTGCTCA 245
Qy 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAAAATTGGCCATAAAACGAGATTAGAG 120
Db 246 CGCGTGTCTTCTGGTGGCTCAATCCCTTGTTTAAAAATTGGCCATAAAACGAGATTAGAG 305
Qy 121 GAAGATCATATGATATTCAGTGTGCCAGAGAACCGCTCACAGCACCTTTGGAGAGAGTTG 180
Db 306 GAAGATCATATGATATTCAGTGTGCCAGAGAACCGCTCACAGCACCTTTGGAGAGAGTTG 365
Qy 181 CAAGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAACCTTCTTTA 240
Db 366 CAAGGTTCTGGGATAAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAACCTTCTTTA 425
Qy 241 ACAAGACAACATATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTAAATTTT 360
Db 426 ACAAGACAACATATAAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTAAATTTT 485
Qy 301 ATTGAGGAAAGTGCACAAAGTAATCCAGCCCAATATTTTGGGAAATTTTAAATTTT 360
Db 486 ATTGAGGAAAGTGCACAAAGTAATCCAGCCCAATATTTTGGGAAATTTTAAATTTT 545
Qy 361 GAAAAATTATATCCCATGGAATTCGTGGCTTTGAAACACAGGCTACGCTATGCCACGGTG 420
Db 546 GAAAAATTATATCCCATGGAATTCGTGGCTTTGAAACACAGGCTACGCTATGCCACGGTG 605
Qy 421 CTGACTTTTTCAGCGCTCATTTTGGCTATCTGCTATCTGCTATCTATTTTATCAGTTCCAG 480
Db 606 CTGACTTTTTCAGCGCTCATTTTGGCTATCTGCTATCTGCTATCTATTTTATCAGTTCCAG 665
Qy 481 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGCGACTTCGT 540
Db 666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGCGACTTCGT 725
Qy 541 CTTAGTAAACATGGCCATGCGGGAAGAGAACACACAGGCCAGATAGTCAATCTGCTGCCAAT 600
Db 726 CTTAGTAAACATGGCCATGCGGGAAGAGAACACACAGGCCAGATAGTCAATCTGCTGCCAAT 785
Qy 601 GATCTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCCCTGCGGAGGACCACTG 660
Db 786 GATCTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCCCTGCGGAGGACCACTG 845
Qy 661 CAGCGCATCGCAGTACTGCCCTACTCTGGAATGAGATAGGAATATCGTCTTGTCTGGG 720
Db 846 CAGCGCATCGCAGTACTGCCCTACTCTGGAATGAGATAGGAATATCGTCTTGTCTGGG 905
Qy 721 ATGCGAGTCTTAATCATTTCTCGCCCTTGCAGAAAGCTGTTTGGGAAAGTTGTTCTCATCA 780
Db 906 ATGCGAGTCTTAATCATTTCTCGCCCTTGCAGAAAGCTGTTTGGGAAAGTTGTTCTCATCA 965
Qy 781 CTGAGGAGTAAACTGCAACTTTTTCAGCGATGCCAGGATCAGGACCATGAATGAAGTTATA 840
Db 966 CTGAGGAGTAAACTGCAACTTTTTCAGCGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025
Qy 841 ACTGGTATAAGGATAATAAAAAATGACCGCTCGGAAAAAGTCATTTTCAAAATCTTATTACC 900
Db 1026 ACTGGTATAAGGATAATAAAAAATGACCGCTCGGAAAAAGTCATTTTCAAAATCTTATTACC 1085
Qy 901 AATTGAGAAAGAGGAGATTTCAGAAATTCCTGAGAAAGTTCTGCTCCCTCAGGGGATGAAT 960
Db 1086 AATTGAGAAAGAGGAGATTTCAGAAATTCCTGAGAAAGTTCTGCTCCCTCAGGGGATGAAT 1145

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QY 961 TTGGCTTCGTTTTTTCAGTGCAGCAAAATCATCGTGTGTTGTGACCTTACCACCTACGTG 1020  
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QY 1021 CTCCTCGGCAGTGTGATCACAGCCAGCGCGGTGTTCTGGCAGTGCAGCTGTATGGGGCT 1080  
Db 1206 CTCCTCGGCAGTGTGATCACAGCCAGCGCGGTGTTCTGGCAGTGCAGCTGTATGGGGCT 1265  
QY 1081 GTGCGGTGACGGTTACCTCTTCTTCCCTCAGCCATTCAGAGGGTGTTCAGAGGCAATC 1140  
Db 1266 GTGCGGTGACGGTTACCTCTTCTTCCCTCAGCCATTCAGAGGGTGTTCAGAGGCAATC 1325  
QY 1141 GTCAGCATCCGAGAAATCCAGACCTTTTGTCTACTTCATGATGATATCACAGCCGAACTG 1200  
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QY 1261 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTACTGTCAGACTGGCGAAATG 1320  
Db 1446 AAGGCATCAGAGACCCCAACTCTACAAGGCTTTTCTTTACTGTCAGACTGGCGAAATG 1505  
QY 1321 TTAGCTGTGTCGGCCCGTGGGAGCAGGAAAGTCATCATCTGTTAAGTGCCTGCTCGG 1380  
Db 1506 TTAGCTGTGTCGGCCCGTGGGAGCAGGAAAGTCATCATCTGTTAAGTGCCTGCTCGG 1565  
QY 1381 GAATTTGGCCCCAAGTCACGGGCTGGTCAGCGTGATGGAAGAAATGGCTATGTCTCAG 1440  
Db 1566 GAATTTGGCCCCAAGTCACGGGCTGGTCAGCGTGATGGAAGAAATGGCTATGTCTCAG 1625  
QY 1441 CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500  
Db 1626 CAGCCCTGGGTGTTCTCGGAACTCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685  
QY 1501 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTTG 1560  
Db 1686 AAGGAACGATATGAAAAGTCATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTTG 1745  
QY 1561 GAGGATGGTATCTGACTGTATAGGAGATCGGGGAACCACTGAGTGGAGGGCAGAAA 1620  
Db 1746 GAGGATGGTATCTGACTGTATAGGAGATCGGGGAACCACTGAGTGGAGGGCAGAAA 1805  
QY 1621 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGGACGAT 1680  
Db 1806 GCACGGGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGGACGAT 1865  
QY 1681 CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740  
Db 1866 CCTCTCAGTCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925  
QY 1741 ATTTTGCATGAGAAATCACAATTTTATGTAAGTCACTCATCAGTTGCACTACCTCAAACTGCA 1800  
Db 1926 ATTTTGCATGAGAAATCACAATTTTATGTAAGTCACTCATCAGTTGCACTACCTCAAACTGCA 1985  
QY 1801 AGTCAGATTTCTGATATTGAAAGATGGTAAATATGTTGCAAGAGGGAATTACACTGAGTTC 1860  
Db 1986 AGTCAGATTTCTGATATTGAAAGATGGTAAATATGTTGCAAGAGGGAATTACACTGAGTTC 2045  
QY 1861 CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA 1920  
Db 2046 CTAATAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAGTGAACAA 2105  
QY 1921 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGGTTTGG 1980  
Db 2106 CCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTTCGGTTTGG 2165  
QY 1981 TCTCAACAAATCTTTCAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCCAAGATACAGAG 2040  
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QY 2041 AATGTCCTCCAGTTACATATCAGAGGAGAACCGTTTCTGAAGAAAAGTTGGTTTTTCAGGCC 2100  
Db 2226 AATGTCCTCCAGTTACATATCAGAGGAGAACCGTTTCTGAAGAAAAGTTGGTTTTTCAGGCC 2285  
QY 2101 TATAAGAAATTTACTTTCAGAGCTGGTGTCTCACTGGATGTTCTTTCATTTTCTTATTTCTCCTA 2160  
Db 2286 TATAAGAAATTTACTTTCAGAGCTGGTGTCTCACTGGATGTTCTTCAATTTTCTTATTTCTCCTA 2345  
QY 2161 AACCTGCACTCAGGTTGCTTATGTCTTCAAGATTTGGTGGCTTTCATCTGCGGCAAC 2220  
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QY 2221 AAACAAAGTATGCTAAATGTCACCTGTAATGAGGAGGAAATGTAACCGAGAGCTAGAT 2280  
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QY 2341 GCAAGATCTCTATTTGGTATTTCTAGTCTTGTAACTCTTCACAAAATTTGCAACAAA 2400  
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QY 2761 GAGAGGTGTCAGGAACCTGTTTGTATGCACACAGGATTTACATTCAGAGGCTTGGTCTTGT 2820  
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QY 2821 TTTTGTGACACGTCCTCGCTGCTGCGCTCCGTCTGGATGCCATCTCTGTCATGTTTGTG 2880  
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QY 3001 GCTGAAGTTCAGAAATATGATGATCTCAGTAGAAAGGGTCAATGTAATACAGACCTTGAA 3060  
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QY 3121 ATAATCTTTGACAAATGTGAACCTTTCATGTACAGTCCAGGTGGGCTCTCTGGTACTGAAGCAT 3180



Db	3306	ATAATCTTTGCAATGTGAACCTTCATGTACAGTCCAGGTGGCCCTCTGCTACTGAAGCAT	3365
Qy	3181	CTGACAGCACTCATTAATCAAGAAAGGTGTGCTATTGGGAAGAACCGGAGCTGGA	3240
Db	3366	CTGACAGCACTCATTAATCAAGAAAGGTGTGCTATTGGGAAGAACCGGAGCTGGA	3425
Qy	3241	AAAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTGAGAACCCGAGGTAAATTTGGATT	3300
Db	3426	AAAAAGTTCCCTCATCTCAGCCCTTTTATAGATTGTGAGAACCCGAGGTAAATTTGGATT	3485
Qy	3301	GATAAGATCTTGACACACTGAAATTTGCACTTCAAGATTTAAGGAAGAAAATGTCAATCAT	3360
Db	3486	GATAAGATCTTGACACACTGAAATTTGCACTTCAAGATTTAAGGAAGAAAATGTCAATCAT	3545
Qy	3361	CCTCAGGAACCTGTGTTTGTTCACCTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG	3420
Db	3546	CCTCAGGAACCTGTGTTTGTTCACCTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG	3605
Qy	3421	CACACGGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA	3480
Db	3606	CACACGGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTGAA	3665
Qy	3481	GATCTTCTGTTAAATGATGATGAACTAGCAGAAATCAGGATCCAAATTTTAGTGTGGA	3540
Db	3666	GATCTTCTGTTAAATGATGATGAACTAGCAGAAATCAGGATCCAAATTTTAGTGTGGA	3725
Qy	3541	CAAGACAACTGTGCTGCTGCGCAGGCAATCTCAGGAAATCAGATATGATTAATT	3600
Db	3726	CAAGACAACTGTGCTGCTGCGCAGGCAATCTCAGGAAATCAGATATGATTAATT	3785
Qy	3601	GATGAAGCGCGCAATGTGGATCCAGAACTGATGATTAATCAAAAAAAATCCGG	3660
Db	3786	GATGAAGCGCGCAATGTGGATCCAGAACTGATGATTAATCAAAAAAAATCCGG	3844
Qy	3661	GAGAAATTTGCCCACTGCAACCGTGTCTAACCATTCGACACAGATTTGAACCAATTTGAC	3720
Db	3845	GAGAAATTTGCCCACTGCAACCGTGTCTAACCATTCGACACAGATTTGAACCAATTTGAC	3904
Qy	3721	AGCGACAAGATATGTTTATAGATTCAGGAGACTGAAAGAAATATGATGAGCCGTATGTT	3780
Db	3905	AGCGACAAGATATGTTTATAGATTCAGGAGACTGAAAGAAATATGATGAGCCGTATGTT	3964
Qy	3781	TTGCTGCAAAATTAAGAGAGCTTATTTTACAAGATGGTGCAACCACTGGGCAAGGCAGAA	3840
Db	3965	TTGCTGCAAAATTAAGAGAGCTTATTTTACAAGATGGTGCAACCACTGGGCAAGGCAGAA	4024
Qy	3841	GCCTGCTCCCTCACTGAAAACAGCAAAACAGGTATATTTCAAAAGAAATTTATCCACATATT	3900
Db	4025	GCCTGCTCCCTCACTGAAAACAGCAAAACAGGTATATTTCAAAAGAAATTTATCCACATATT	4084
Qy	3901	GGTCACACTGACACATGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACCTATT	3960
Db	4085	GGTCACACTGACACATGTTTACAAACACTTCCAAATGGACAGCCCTCGACCTTAACCTATT	4144
Qy	3961	TTGAGACAGCACTGTGA	3978
Db	4145	TTGAGACAGCACTGTGA	4162

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2005, 03:10:37 ; Search time 12057 Seconds  
(without alignments)  
12558.652 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtcgccgtgtaccagga.....ttttcagacagcactgtga 3978

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_est8:\*

9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3322.2	83.5	3685	9 AY415506	AY415506 Homo sapi
2	2741.4	68.9	4594	3 AK052778	AK052778 Mus muscu
3	2719.4	68.4	3685	9 AY415507	AY415507 Pan trogl
4	2289.8	57.6	3679	9 AY415508	AY415508 Mus muscu
5	1237.2	31.1	3208	3 AK032802	AK032802 Mus muscu
6	734	18.5	1084	4 BM462073	BM462073 AGENCOURT
7	725	18.2	915	5 BP382967	BP382967 AGENCOURT
8	717.4	18.0	747	7 CF597322	CF597322 AGENCOURT
9	712.8	17.9	797	6 CD657554	CD657554 AGENCOURT
10	703.6	17.7	1679	3 CR704782	CR704782 Tetraodon
11	665.6	16.7	810	7 CF786044	CF786044 AGENCOURT
12	660.2	16.6	951	5 BU186494	BU186494 AGENCOURT
13	638	16.0	682	2 BB879353	BB879353 601484613
14	634	15.9	639	7 CN410192	CN410192 170006000
15	620.4	15.6	865	7 CK776984	CK776984 966272 MA
16	620.4	15.6	1503	3 CR683466	CR683466 Tetraodon
17	614	15.4	727	2 BE879718	BE879718 601491617
18	605.8	15.2	1139	5 BQ069612	BQ069612 AGENCOURT
19	583	14.7	583	5 BP292935	BP292935 BP292935
20	582.8	14.7	689	4 BI771442	BI771442 603059489
21	565.4	14.2	896	5 BQ889997	BQ889997 AGENCOURT
22	553.8	13.9	852	1 AJ814701	AJ814701 AJ814701
23	546	13.7	926	2 BE885514	BE885514 601508707
24	542.2	13.6	581	5 BP379624	BP379624 BP379624

25	535.6	13.5	702	6	CB451973	CB451973 706792 MA
26	521	13.1	663	6	CB452140	CB452140 706984 MA
27	502.4	12.6	761	7	CN537837	CN537837 UI-M-HS0-
28	498.4	12.5	716	7	CK837582	CK837582 4062919 B
29	493.2	12.4	706	7	CN793971	CN793971 4129077 B
30	492.6	12.4	710	6	CB169756	CB169756 KSV603161
31	492	12.4	802	5	BU117050	BU117050 603139132
32	491	12.3	491	5	EX474791	EX474791 DKF2686G
33	485	12.2	497	1	AL701816	AL701816 DKF2686F
34	480.6	12.1	733	1	AJ742393	AJ742393 AJ742393
35	470.6	11.8	726	6	CB451559	CB451559 706335 MA
36	469	11.8	478	2	BE674208	BE674208 7D76907.X
37	462.2	11.6	724	1	AJ742392	AJ742392 AJ742392
38	460	11.5	826	1	AJ742388	AJ742388 AJ742388
39	458	11.5	647	7	CN786768	CN786768 4120812 B
40	457.8	11.5	661	7	CK838071	CK838071 4063458 B
41	456.4	11.5	639	2	BB225682	BB225682 BB225682
42	449.6	11.3	679	7	CF169708	CF169708 B0817B02
43	446.4	11.2	4185	9	AY407265	AY407265 Homo sapi
44	446	11.2	4185	9	AY407266	AY407266 Pan trogl
45	445.2	11.2	682	6	CB449596	CB449596 703807 MA

ALIGNMENTS

RESULT 1  
AY415506  
LOCUS Homo sapiens ABCC4 gene, VIRTUAL TRANSCRIPT, partial sequence, 3685 bp DNA linear GSS 17-DEC-2003  
DEFINITION Homo sapiens ABCC4 gene, VIRTUAL TRANSCRIPT, partial sequence, 3685 bp DNA linear GSS 17-DEC-2003  
ACCESSION AY415506  
VERSION AY415506.1 GI:39771465  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3685)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 3685)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source

1. 3685

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/db\_xref="taxon:9606"

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ORIGIN

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Matches 332; Conservative 0; Mismatches 361; Indels 0; Gaps 0;

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RESULT 2  
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 DEFINITION AK052778  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

ACCESSION AK052778  
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 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akizawa, J., Nishii, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Fujimoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yajima, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (baes 1 to 4594)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanganaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, N., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
 Location/Qualifiers  
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 Matches 3185; Conservative 0; Mismatches 721; Indels 1; Gaps 1;  
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Qy	2413	ATTCTGAAGCTCCGGTATTTATCTTTGATAGAAATCCAATAGGAAGATTTTAAATCGT	2472
Db	2506	ATACTGAAGCTCCCGTGTGTTCTTCGACAGAAATCCAATCGGGAGATTTTAAATCGT	2565
Qy	2473	TTCTCCAAAGACATTTGACACTTGGATGATTTGTCGCGCTGACGTTTATGATTTTCAATC	2532
Db	2566	TTCTCCAAAGACATCGGACACATGGATGATTTGCTTCCCTGACGTTTCTGGACTTCATC	2625
Qy	2533	CAGACATTTGCTCAAAAGTGGTGGTCTCTGTGGCTGTGGCCGTGATTTCTTGGATC	2592
Db	2626	CAGAGCTTGTCTCTCGTAAAGTGTGATCGCTGTGCGCGCGCGTATCCCTTGGATC	2685
Qy	2593	GCAATACCTTGGTTCCTTCCCTTGGAAATCATTTTCAATTTTCTTCGCGCAATATTTTGA	2652
Db	2686	CTCATACATTTGGTTCGCTCTCAGTCTGCTTCTCTGCTTCTTCGAGATATCTTCTTAG	2745
Qy	2653	ACGTCAAGAGATGTGAAGCGCTCGAATCTACAACTCGAGTCCAGTGTGTTTCCACATG	2712
Db	2746	ACGTCAAGGATGTCAAGCGCTTGAATCCAAACACGAGCCCGGTATTTCTCCATTTA	2805
Qy	2713	TCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAGGTGTGAG	2772
Db	2806	TCGTCTCTCTCCAGGGGACTCTGGACCATCCGGGCTTACAAAGCTGAGGAGAGGTGTG	2865
Qy	2773	GAACTGTTGATGACACACAGGATTTACATTTACAGAGCTTGGTCTTGTGTTTTCACAACG	2832
Db	2866	GAGCTGTTGATGACACACAGGACTTGCATTTACAGAGCTTGGTCTTGTGTTTTCACAACG	2925
Qy	2833	TCCCGCTGG-TTCGCGCTGCTGATGCCATCTGTGCCATGTTGTTCATCATCTGTTGC	2891
Db	2926	TCGAGATGGTTTCTGTGCTCTGGACGCACTCTGCCCATCTTTGTAATCTGTCGTTGC	2985
Qy	2892	CTTTGGGTCTCTGATTTCTGGCAAACTCTGGATTCGCGGCGAGGTTGGTTTGGCACTGTC	2951
Db	2986	CTTCGGGTCTCTGTTCTGCGGAAGACTTTGMAATGCTGGGCGAGTTGGCTTGGCTTGTG	3045
Qy	2952	CTATGCCCTCACGCTCATGCGGATGTTTCAAGTGTGTGTCGACAAAGTGTGTAAGTTGA	3011
Db	3046	CTAGCCCTCACACTCATGCGGATGTTTCCAGTGTCTGTGCGACAGAGCGCGAAGTAGA	3105
Qy	3012	GAATATGATCATCTCAGTAGAAGGGTCAATTGAATACACAGACCTTGAAGAAGACACC	3071
Db	3106	GAATATGATCATTTCACTGAGAGAGTGTAGTACACGACCTTAGAAGAGGAGCGCC	3165
Qy	3072	TTGGGAATATCAGAAACGCCACACAGCTTGGCCCATGAAAGAGTGAATACTTTGA	3131
Db	3166	TTGGGAGTCAAGNAGCGCCCAACCCCGAGCTGGCCCAACGAGGAGTCTCGTCTTCGA	3225
Qy	3132	CAATGTGAATCTCATGTACAGTCCAGTGGGCTCTGGTACTGAAGCATCTGACAGCACT	3191
Db	3226	CAATGTGAATCTTCACTTACAGCTTAGATGGGCTCTGGTCTGAAAGCACTGACGTGGCT	3285
Qy	3192	CATTAAATCACAAGAAAGGTTGCAATGTTGGNAGAACCGGAGCTCGNAAAAGTTCCT	3251
Db	3286	CATCAAGTCCAGGAAAGGTTGGAATTTGGGCGAAGACCGGAGCTGGGAAAAGCTCCCT	3345
Qy	3252	CATCTCAGCCCTTTTATGATTTGAGAAACCGAGGTAAATTTGGATTTGATAGATCTT	3311
Db	3346	CATCTCGGCTCTTTCAGGCTGTCAAGACCGAGGGGAAATCTGGATCGATAGATCTT	3405
Qy	3312	GACAACTGAATTTGACTTCAAGATTTAAGAAAGAAATGTCAATCATCTACAGGAAC	3371
Db	3406	GACAACTGAATTTGAGCTTCAAGCTTAAAGAAAGAAATGTCAATCATCTACAGGAAC	3465
Qy	3372	TGTTTGTTCACCTGGAACATGAGGAAACCTGGATCCCTTTAAATGAGCACACGGATGA	3431
Db	3466	TGTTTGTTCACCTGGAACATGAGGAAACCTGGATCCCTTTAAATGAGCACACGGATGA	3525
Qy	3432	GGAACTGTGGAATGCTTACAGAGGTACAACTTAAAGAAACCATTTGAAGATCTTCTCGG	3491
Db	3526	GGAGCTGTGAGGGCTTGGAGGAGGTACAACTTAAAGAGGCAATTTGAAGATCTTCTCGG	3585
Qy	3492	TAAAAATGGAATCTGAATTTAGCAGAACTCAGGATCCAAATTTTGTGTTGGACAAAGCACT	3551
Db	3586	AAAAATGGAATCTGAATTTAGCAGAACTCAGGATCCAAATTTTGTGTTGGACAGACAGT	3645
Qy	3552	GGTGTGCTTGCAGGGCAATTTCTCAGGAAATCTCAGATATTTGATTTGATGAGGAC	3611
Db	3646	AGTGTGCTTGCAGGGCCATTTCTAAAGAAATACCGAATACTGATCATTTGATGAGCAAC	3705





Qy 1266 ATCAGAGACCCCAACTCTACAAGGCTTTTCTTTATCTGTCTAGACCTGGCGAATTGTTAGC 1325  
Db 1081 ATCAGAGACCCCAACTCTACAAGGCTTTTCTTTACTGTCTAGACCTGGCGAATTGTTAGC 1140  
Qy 1326 TGTGGTCGGCCCGTGGAGCAGGAGTCTACTGTTAAGTCCGCTCGGGGAATT 1385  
Db 1141 TGTGGTCGGCCCGTGGAGCAGGGAAGTCTACTGTTAAGTCCGCTCGGGGAATT 1200  
Qy 1386 GGGCCCAAGTCA CGGGCTGGT CAGCGTGCATGGAAGAAATGCCATATGTCTCAGCAGCC 1445  
Db 1201 GGGCCCAAGTCA CGGGCTGGT CAGCGTGCATGGAAGAAATGCCATATGTCTCAGCAGCC 1260  
Qy 1446 CTGGGTGTTCTCGGAACTCTGAGAGTAATATTTATTTTCGGGAAGAAATACGAAAAGGA 1505  
Db 1261 CTGGGTGTTCTCGGAACTCTGAGAGTAATATTTATTTTCGGGAAGAAATACGAAAAGGA 1320  
Qy 1506 ACGATATGAAAAGTCAATAAGGCTTGTCTCTGAAAAGAAATTTACAGCTGTTGGAGGA 1565  
Db 1321 ACGATATGAAAAGTCAATAAGGCTTGTCTCTGAAAAGAAATTTACAGCTGTTGGAGGA 1380  
Qy 1566 TGGTGATCTGACTGTGATAGGATCGGGGAACCA CGCTGAGTGGAGGGCAGAAAAGCAAG 1625  
Db 1381 NNN 1440  
Qy 1626 GGTAAACCTTGCAGAGCAGGTATCAAGATGCTGACATCTATCTCTGGACGATCTCT 1685  
Db 1441 NNN 1500  
Qy 1686 CAGTGCAGTAGATCGGGAAGTTACAGACACTTGTTCGAACGTGTATTTGTCAAATTTT 1745  
Db 1501 CAGTGNNNNNNTCGGAAGTTAGCAGACACTTGTTCGAACGTGTATTTGTCAAACCTTT 1560  
Qy 1746 GCATGAGAAGATCAAAATTTTAGTGACTCATCAGTTGCAAGTCTCAAAGTCAAGTCA 1805  
Db 1561 GCATGAGAAGATCAAAATTTTAGTGACTCATCAGTTGCAAGTCTCAAAGTCAAGTCA 1620  
Qy 1806 GATTCTGATATGAAAGATGTAATAATGGTGCAAGGGGACTTTACACTGATTCCTAAA 1865  
Db 1621 GATTCTGATATGAAAGATGTAATAATGGTGCAAGGGGACTTTACACTGATTCCTAAA 1680  
Qy 1866 ATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATAAGAGGAAAGTGAACACCTCC 1925  
Db 1681 ATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGACAACAGAGAAAGTGAACACCTCC 1740  
Qy 1926 AGTTCCAGGAATCCCACTAAGAAATCGTACCTCTCAGAGTCTTCGGTTTGGTCTCA 1985  
Db 1741 AGTTCCAGGAATCCCACTAAGAAATCGTACCTCTCAGAGTCTTCGGTTTGGTCTCA 1800  
Qy 1986 ACAATCTTAGACCTCTTTGAAAGATGGTGTCTCTGGAGGCAAGATACAGAGAATGT 2045  
Db 1801 ACAATCTTAGACCTCTTTGAAAGATGGTGTCTCTGGAGGCAAGATACAGAGAATGT 1860  
Qy 2046 CCCAGTTACTATCAGAGGAAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCTATAA 2105  
Db 1861 CCCAGTTACTATCAGAGGAAACCGTTCTGAAAGAAAGTTGGTTTTCAGGCTATAA 1920  
Qy 2106 GAATTAATTCAGAGCTGTGCTCACTGATGTCTTCAATTTTCTTATTTCTCTTAAACAC 2165  
Db 1921 GAATTAATTCAGAGCTGTGCTCACTGATGTCTTCAATTTTCTTATTTCTCTTAAACAC 1980  
Qy 2166 TGCAGCTCAGGTGCTATGTCTTCAAGATTTGGTGGCTTTTCACTGGGCAAAACAAACA 2225  
Db 1981 TGCAGCTCAGGTGCTATGTCTTCAAGATTTGGTGGCTTTTCACTGGGCAAAACAAACA 2040  
Qy 2226 AAGTATGCTAAATGCTGTAAATGGAAGGAAATGTAAACCGAAGCTAGATCTTTAA 2285  
Db 2041 AAGTATGCTAAATGCTGTAAATGGAAGGAAATGTAAACCGAAGCTAGATCTTTAA 2100  
Qy 2286 CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTCTTTTGGCATAGCAAG 2345  
Db 2101 CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTCTTTTGGCATAGCAAG 2160  
Qy 2346 ATCTCTATTGGTATTTCTACGTCCTTGTAACTCTTCAAACTTTTGCAACAAATGTT 2405

Db 2161 ATCTCTATTGGTATTTCTACGTCCTTGTAACTCTTTCACAACTTTGCACAAACAAATGTT 2220  
Qy 2406 TGAGTCAATTTCTGAAAGCTCGGTATTTATTTCTTTGATAGAAATCCAATAGGAAGAAATTTT 2465  
Db 2221 TGAGTCAATTTCTGAAAGCTCGGTATTTATTTCTTTGATAGAAATCCAATAGGAAGAAATTTT 2280  
Qy 2466 AAATCGTTTTCTCCAAAGACATTTGACACTTTGGATGATTTGCTGCCGTGAGCGTTTTAGA 2525  
Db 2281 AAATCGTTTTCTCCAAAGACATTTGACACTTTGGATGATTTGCTGCCGTGAGCGTTTTAGA 2340  
Qy 2526 TTTTCATCCAGACATTTGCTAACAGTGGTGTGGTCTCTGTGGCTGTGGCGGTGATTTCC 2585  
Db 2341 TTTTCATCCAGNNNTTGTCTACAAAGTGGTGTGGTCTCTGTGGCTGTGGCGGTGATTTCC 2400  
Qy 2586 TTTGGATCGCAATACCTTGGTTCCTTGGATCAATTTTCAATTTCTTCCGCCGATATTT 2645  
Db 2401 TTTGGATCGCAATACCTTGGTTCCTTGGATCAATTTTCAATTTCTTCCGCCGATATTT 2460  
Qy 2646 TTTGGAAACGTCAAGAGATGTGAAGCGCTTGGAAATCTACAACTCGGAGTCCAGTGTTTTC 2705  
Db 2461 TTTGGAAACGTCAAGAGATGTGAAGCGCTTGGAAATCTACAACTCGGAGTCCAGTGTTTTC 2520  
Qy 2706 CCATTTCTCATCTTCTCTCCAGGGGCTCTGGAACCATCCGGGCATACAAAGCAGAAGAG 2765  
Db 2521 CCATTTATCATCTTCTCTCCAGGGGCTCTGGAACCATCCGGGCATACAAAGCAGAAGAG 2580  
Qy 2766 GTGTCCAGGAATCTTTTCAATGACACACAGGATTTTACATTCAGAGGCTTGGTTCTTGTTTT 2825  
Db 2581 GTGTCCAGGAATCTTTTCAATGACACACAGGATTTTACATTCAGAGGCTTGGTTCTTGTTTT 2640  
Qy 2826 GACAACTCCCGCTGGTTCGCGCTCTGGATGCCATCTGTGCCATGTTTGTTCATCAT 2885  
Db 2641 GACAACTCCCGCTGGTTCGCGCTCTGGATGCCATCTGTGCCATGTTTGTTCATCAT 2700  
Qy 2886 CGTTGCCCTTTGGGTCCCTGATTTCTGGCAAAAACCTCTGGATGCCAGGTTGGTTGGC 2945  
Db 2701 CGTTGCCCTTTGGGTCCCTGATTTCTGGCAAAAACCTCTGGATGCCAGGTTGGTTGGC 2760  
Qy 2946 ACTGTCTATGCTCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTCTCGACAAAGTCTGA 3005  
Db 2761 ACTGTCTATGCTCCCTCAGCTCATGGGGATGTTTTCAGTGGTGTCTCGACAAAGTCTGA 2820  
Qy 3006 AGTTGAGAATATGATGATCTCAGTAGAAAGGTCATTTGAATACACAGACCTTTGAAAAGA 3065  
Db 2821 AGTTGAGAATATGATGATCTCAGTAGAAAGGTCATTTGAATACACAGACCTTTGAAAAGA 2880  
Qy 3066 AGCACTTTGGGAATATCAGAAAACGCCCAACCGGCTGGCCCCATGAAAGGATGATAAT 3125  
Db 2881 AGCACTTTGGGAATATCAGAAAACGCCCAACCGGCTGGCCCCATGAAAGGATGATAAT 2940  
Qy 3126 CTTTGAATATGTAATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3185  
Db 2941 CTTTGAATATGTAATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
Qy 3186 AGCACTCATTTAAATACAAAGAAAAGTTGGCATTTGTGGGAAGAACCGGAGCTGGAAGA 3245  
Db 3001 AGCACTCATTTAAATACAAAGAAAAGTTGGCATTTGTGGGAAGAACCGGAGCTGGAAGA 3060  
Qy 3246 TTCCCTCATCTCAGCCCTTTTATGATTTGTGAGAACCCGAAAGGTTAAATTTGGATTTGATA 3305  
Db 3061 NNN 3120  
Qy 3306 GATCTTGACAACTGAAATTTGGCATTTGAGGAAAGAAATGTCAATCATACCTCA 3365  
Db 3121 NNN 3180  
Qy 3366 GGAACCTGTTTGTCTACTGAAACAAATGAGAAAACCTGGATCCCTTTTAAATAGACAC 3425  
Db 3181 NGAACCTGTTTGTCTACTGAAACAAATGAGAAAACCTGGATCCCTTTTAAATAGACAC 3240  
Qy 3426 GGAATGAGGAATCTGTGGAATCCCTTTAAGAGGTTCAACTTAAAGAAACCAATTTGAAGATCT 3485



Db 1016 ACCATCTGATGGCAAGCCATTGTCCAGTCGTCAGAGATTTACCGCTTTCTGGGCAAGGC 1075  
Qy 1266 ATCAGAGACCCCAACTCTCAAGGCTTTTCTTTACTGTCAAGCTCGCGAATTTGTAGC 1325  
Db 1076 ACTAGACAGTCCAACTCTGCAAGGCTTTCTTTATTATGCCAGACTGGTGAATTTGTAGC 1135  
Qy 1326 TGTGCTGGCCCGCTGGGAGCAGGAGTCACTGTTTAAAGTCGCTCGGGGAATT 1385  
Db 1136 CGTGGTTGGCCCACTTGGAGCAGGCAAGTCGCTGTGAGCGCAGTCTGGGTGAGCT 1195  
Qy 1386 GGCCCCAAGTCACCGGCTGGTCAAGTCGTCAGGAGAAATTCCTATGTCCTCAGCAGCC 1445  
Db 1196 GCTTCTGCGAGCGGCTGGTCAAGTCGTCAGGAGAAATTCCTATGTCCTCAGCAGCC 1255  
Qy 1446 CTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATTTATTTTGGGAGAAATACGAAAGGA 1505  
Db 1256 CTGGGTGTTCTCGGGAACCTCTGAGGAGCAATTTTATTTGGGAGAAATATGAGAAGGA 1315  
Qy 1506 ACGATATGAAAGTCAATAAGGCTTGTCTCTGAAAGGAATTTACAGCTGTTGGAGGA 1565  
Db 1316 GCGATATGAGAAAGTCAAGGCTTGTCTCTGAAAGGAACCTGAGCTTCTGGAGGA 1375  
Qy 1566 TGGTATCTGACTGTAGTAGAGATCGGGGAACCAAGCTGAGTCGAGGGCAGAAAGCAGC 1625  
Db 1376 CGGGGATCTGACGGTATAGGAGACCGGGGAGCCACGCTGAGTCGAGGCGCAGAAAGCTCG 1435  
Qy 1626 GGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGAACGATCTCT 1685  
Db 1436 GGTGAACTTGGCAGCGGCTGTACAGGAGCGCGACATCTACTCTCTTGTATGATCGCT 1495  
Qy 1686 CAGTGCAGTATGATCGGAAGTTAGCAGACACTTGTCTCGAACTGTATTTGTCAAAATTTT 1745  
Db 1496 CAGCGCTGTGATGCAAGATGGGCAAGCACCCTGTCCAACTGTGTATCTGTCAAGCGGTT 1555  
Qy 1746 GCATGAGAGATCAAAATTTAGTACTCATCAGTTGAGTACTCAAGCTGCAAGTCA 1805  
Db 1556 GCAGGAGAGATCAAAATTTAGTACTCATCAGTTGAGTACTCAAGCTGCAAGCTCA 1615  
Qy 1806 GATTCTGATATTGAAGATGTAATAATGTCAGAGGGAATTTACACTGATGTTCTTAA 1865  
Db 1616 CATCTCATACTAAGATGTAAGATGTCAGAGGGAATTTACAGGGAATTTCTGAA 1675  
Qy 1866 ATCTGATATGATTTGGCTCCCTTTTAAAGAGGTAATGAGGAAAGTGAACAACTCC 1925  
Db 1676 ATCTGATGATATTGGCTCCCTTTTAAAGAGGTAATGAGGGAATTTCTGAA 1675  
Qy 1926 AGTTCAGGAACTCCACACTAAGGATCGTACCTTCTCAGAGTCTCGGTTGGTCTCA 1985  
Db 1736 AGCCCCAGGAAACCCGACACTCAGGAAACGAACTTCTCGAGGCTCAATTTGGTCTCA 1795  
Qy 1986 ACAATCTCTAGACCTCTTGAAGATGGTCTCTGAGAGCCCAAGATACAGAGAATGT 2045  
Db 1796 GCAGTATCCAGACCTCTGTTGAAGAGCGGGGCCCAAGGGCCCAAGCAGAGAAACAC 1855  
Qy 2046 CCCAGTTTACACTATCAGAGGAGAACCGTCTGGAAGGAAAGTGGTTTTTCAGGCTTAA 2105  
Db 1856 GCAGCAGTGCACCCGAGGAGACCGTTCGGAAGGAGGAATCGCTTCAAGGCTTACAA 1915  
Qy 2106 GAATTAATCTCAGAGCTGGGTCTCACTGGAATGCTTCTTCAATTTCTTATCTCTTAAACAC 2165  
Db 1916 GAATTAATCTCTCGGCGGGCGCATCTCGTTCATCATTTCTCTGCTGTCTTAAAT 1975  
Qy 2166 TGCAGCTCAGTGTGCTTCAAGATGGTGGCTTCTATCTGAGGCAACAAACA 2225  
Db 1976 GGTGGCCAGGTTTCTATGTTCTTCAAGGACTGGTGGCTTTCCACCTGGGCGAACAGCA 2035  
Qy 2226 AAGTATCTCTAAATGCTGTAATGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAA 2285  
Db 2036 AGGTGACTGACAAACCAAGAAATGGAATGGAATATTAACGAGACCTTAGACCTCAG 2095  
Qy 2286 CTGCTACTAGGAATTTATCAGGTTTAACTGTAAGTACCTGCTTTTGGCATAGCAAG 2345  
Db 2096 CTGCTACTAGGAATTTACGAGGCTTAACTGCGGTCACCGTCTCTTTTGGCATAGCGAG 2155

Qy 2346 ATCTCTATTTGTTATTTACGTCCTTTGTTAACTCTTCAAACTTTGCACAAACAAATGTT 2405  
Db 2156 ATCCCTACTGGTGTCTTATATCTTGTGAAGCTTCCAGACTTTTGACAAACAGATGTT 2215  
Qy 2406 TGAGTCAATTTCTGAAGCTCGGTATTTATTTCTTTGATAGAAATCAATAGGAAGATTTT 2465  
Db 2216 TGAGTCATATCTGAAGCTCCGCTGTTGTTCTTTTGACAGAAATCAATCGGAGGATTTT 2275  
Qy 2466 AAATCGTTTTCTCAAAGACATTTGACACTTTGGATGTTTGTGCGCTGAGCTTTTGA 2525  
Db 2276 AAATCGTTTTCTCAAAGACATTTGACACTTTGGATGTTTGTGCGCTGAGCTTTTGA 2335  
Qy 2526 TTTTCATCCAGACATTTGTACAAAGTGGTGTGCTCTCTGTGCTGTGGCCGCTGATTC 2585  
Db 2336 CTTTCATCCAGACGTTGCTCTCTGCTGTAAGTGTGATCGCTGTGCGCGCGGCTGATCC 2395  
Qy 2586 TTGATCGCAATACCTTTGGTTCCTTTGGAATCATTTTCATTTTCTTCGCGCATATTT 2645  
Db 2396 TTGATCTCTCATACATTTGGTTCGCTCTCAGTCTCTCTGCTGTTCTTCGAGATACTT 2455  
Qy 2646 TTTGGAAACGTCAGAGATGTGAAGCGCTGGAATCTACACTCGGAGTCCAGTGTTC 2705  
Db 2456 CTTAGAGACGTCAGGGATGTCAAGCGCTGGAATCCAC-ACAGGAGCCCGTATTCCT 2514  
Qy 2706 CCATCTGTCATCTTCTCCAGGGCTCTGGAACCATCGGGCATACAAAGCAGAGAGAG 2765  
Db 2515 CCATTTATCTCTCTCCAGGACTCTGGAACCATCGGGCTTACAAAGCTGAGGAGAG 2574  
Qy 2766 GTGTCAGAACTGTTTGTATGCACACAGGATTTACATTCAGAGGCTTGGTTCCTTTT 2825  
Db 2575 GTGTCAGAGCTGTTTGTATGCACACAGGACTTGCATTTAGAGGCTTGGTTCCTTCT 2634  
Qy 2826 GACAACTCTCGCTGGTTCGCTCTGGAATCGCTCTGGAATCGCTGTCGCTGTCATCAT 2885  
Db 2635 GAGCATCATGAGATGGTTCGCTCTGGAATCGCTGTCGCTGTCGCTGTCATCATCGT 2694  
Qy 2886 CGTTGCTTTGGGTCCTGATTTGCGCAAACTCTGGAATCGCTGCGGAGGTTGGTTCG 2945  
Db 2695 CGTTGCTTTGGGTCCTGATTTGCGCAAACTCTGGAATCGCTGCGGAGGTTGGCTGGC 2754  
Qy 2946 ACTGCTCTATGCTCTCAGCTCATGCGGATGTTTCACTGCTGCTGTCGCAAAAGTCTGA 3005  
Db 2755 CTTGCTCTAGCTCTCAGCTCATGCGGATGTTTCACTGCTGCTGTCGCAAGAGGCTG 2814  
Qy 3006 AGTTGAAATATGATGATCTCAGTGAAGAGGTCATTTGAATACACAGACCTTGAAGA 3065  
Db 2815 AGTAGAATATGATGATTTTCACTGGAAGAGTGAATGAGTACACGACCTTAGAGA 2874  
Qy 3066 AGCACTTTGGGAATATCAGAAACGCCCAACCAAGCTGCGCCCATCAAGAGGATGATA 3125  
Db 2875 GGCGCTTTGGAGTGCAAGAGCGCCCAACCCAGGCTGCGCCCAAGGAGTCTATCGT 2934  
Qy 3126 CTTTGAATATGAACTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 3185  
Db 2935 CTTTGAATATGAACTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2994  
Qy 3186 AGCACTTAAATCAACAGAAAGGTTGGATTTGTTGGGAGAAACCGGAGCTGGAAGA 3245  
Db 2995 TGGGCTCATCAAGTCCAGGGAAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3054  
Qy 3246 TTCCCTCATCTCAGCCCTTTTATGTTTGCAGAAACCCGAAAGGTTAAATTTGGATT 3305  
Db 3055 NNN 3114  
Qy 3306 GATCTTTGACAACTGAAATTTGAGCTTTCAGATTTAAGGAAGAAATGTCATATAC 3365  
Db 3115 NNN 3174  
Qy 3366 GGAACCTGTTTGTCTGGAACATGAGGAAACCTGGAATCCCTTTTATGAGACAC 3425  
Db 3175 NGAACCTGTTCTGTTCACTGGAACCATGAGGAAACCTGGAACCTTCAATGAGCAC 3234



Db	122	CCAAATCGGGAGATTTTAAATCGTTTCTCTCAAAGACATCGGACACATGGATGATTTGCTT	181
Qy	2509	CCGCTGACGTTTTTATAGATTTTCATCCAGACATTTGCTTCAAGTGGTTGGTGTGCTCTCTGTG	2568
Db	182	CCCCCTGACGTTTCCCTGGACTTCATCCAGACGTTGCTCTCTCGTAAAGTGTGATCGCTGTG	241
Qy	2569	GCTGTGGCCGTGATTCCTTTGGATCGCAATACCCCTTGGTTCCCTTGGATCAATTTTCATT	2628
Db	242	CCCGCGCCGCGTATCCCTTGGATCCCTATACCATTTGGTTCCGCTCTCAGTCGTCGCTTCC	301
Qy	2629	TTTCTTTCCGCGATATTTTTCGAAACGTCGAAGATGTGAAGCGCCTGGAAATCTFACAAC	2688
Db	302	GTTCTTTCGGAGATACTTCTTAGAGACGTCACGGATGTCAAGCGCTGGAAATCCACAACA	361
Qy	2689	CGGAGTCCAGTGTGTTTCCCACCTGTTCATTTCTCTCCAGGGGCTCTGGACCAATCCGGCA	2748
Db	362	CGGAGCCGGTATTCTCCCATTTTATCGTCTCTCCCTCCAGGGACTCTGGACCAATCCGGCT	421
Qy	2749	TACAAAGCAAGAGAGAGGTGTCAGGACTGTTTTCATGTCACACACAGGATTTACATTCAGAG	2808
Db	422	TACAAAGCTGAGGAGAGGTGTCAGGAGCTGTTTGAATGCACACCAAGACTTGTCAATTCAGAG	481
Qy	2809	GCTTGGTTCTTGTGTTTTCGACAAAGTCCCGCTGGTTTCGCGCTCGCTCGGAATGCCATCTGT	2868
Db	482	GCTTGGTTCTTGTGTTTTCGACACATCGAGATGGTTCGCTGCGCTCTGAGCGCCATCTGC	541
Qy	2869	GCCATGTTTGTCAATCATCGTTTGGCTTTGGGTCCTCGATTTCTGGCNAAAACTCTGGATGCC	2928
Db	542	GCCATCTTTGTAATCGTGTGCTTCCGCTTCCGCTTCCGCTTCTGGCGAAGACTTGTGAATGCT	601
Qy	2929	GGGACAGTTGTTTGGCACCTGTCCTATGCCCCCTCAAGCTCATGCGGATGTTTTCAGTGTGT	2988
Db	602	GGGACAGTTGGCCCTGGCTTGTCTCAAGCCCCCTCACTCATGCGGGAATGTTCCAGTGTCT	661
Qy	2989	GTTTCGACAAAGTGTCTGAGTTGGAATATGATGATCTCAGTAGAAAGGTCATTTGAATAC	3048
Db	662	GTGCGACAGACGCGCGAAGTAGAGAAATATGATGATTTTCAGTGGAGAGAGTATTTAGTAC	721
Qy	3049	ACAGACCTTTGAAAAAGAACGACCTTTGGGAAATATCAGAAAAAGCCCCACACAGAGCTGCGCC	3108
Db	722	ACGACCTTAGAGAGGAGCGCCTTGGAGTGCAAGAGCGCCACACCCGAGCTGCGCC	781
Qy	3109	CATGAAGAGTGATAATCTTTTGAACAATGTGAATTCATGTACAGTCAGGTGGGCTCTGT	3168
Db	782	CACGAGGAGTCATCGTCTTCGACAAATGTGAATTTCACTACAGCTTAGATGGGCTCTGT	841
Qy	3169	GTACTGAGCATCTGACAGCACTCATTAATATCAAGAAAAGTTGGCATTTGGGGAAGA	3228
Db	842	GTTCTGAAGCACCTTGACTGCGCTCATCAAGTCCAGGGAAAAGTTGGAATTTGGTGGCAGA	901
Qy	3229	ACCGAGCTGGAAGAAAGTTCCCTCATCTCAGCCCTTTTATAGTTGTCAAGAACCCGAAGGT	3288
Db	902	ACCGAGCTGGAAGAAAGTCCCTCATCTCGGCCCTCTTCAGGCTGTACAGAACCCGAGGG	961
Qy	3289	AAAAATTGGATTGATAAGATCTTGACAACTGAATTTGGACTTCACGATTTAAGGAAGAAA	3348
Db	962	AAAAATCGATCGATAAGATCTTGACAAACCGAAATTTGGCTTCACGACTTAAGGAAGAAA	1021
Qy	3349	ATGTCNAATCATCTCAGGAACCTGTTTGTTCATCTGGACAATGAGGAAAAACCTCGAT	3408
Db	1022	ATGTCNAATCATPACACAGGAACCTGTTCTGTGTTCACTGGAAACCAATGAGGAAAAACCTGGAC	1081
Qy	3409	CCCTTTAATGAGCACACGGATGAGGAATCTGTGGAAATGCTTTTACAAGAGGTACAACTTAAA	3468
Db	1082	CCCTTCAATGAGCACACGACGAGAGCTGTGGAGGGCTTTGGAGGAGGTACAACTTAAA	1141
Qy	3469	GAAGAACCAATTTGAAGATCTTCTCGTGTAAAAATGGATACTGAAATTAGCAGGAATCAGGATCCAAT	3528
Db	1142	GAGGCCAATGAAGATCTTCTCGGAAGAAATGGATACTGAAATTAGCAGGAATCTGGATCCAAT	1201
Qy	3529	TTTAGTGTGGAACAAGACAACTCGGTGTGCTTCCGACGGGCAATTTCTCAGAAAAATTCAG	3588
Db	1202	TTCAAGTGTGGAACAGACAGTGTAGTGTGCTTCCGAAAGGCGCAATTTCAAAAAATAACCGA	1261

QY	3589	ATAATTGATTTATGATGAAGCGACGGCAAAATGTGGATCCCAAGAACTGATGAGTTTAATACAA	3648
Db	1262	ATACTGATCATTTGATGATGAAGCAACTGCAAAATGTGGACCCCAAGAACGGATGAGTTTAATACAA	1321
QY	3649	AAAAAATCCGGGAGAAATTTGCCCACTGCGACCGTGTCTAACCAATTCAGAACTGACACAGATTGAAC	3708
Db	1322	CAGAAGATCCGGGAGAAGTTTGGCCAGTGCAAGTGTCTACCAATTCAGAACTGACACAGATTGAAC	1381
QY	3709	ACCATTATTGACAGCGCAAGAATAATAGTTTTCAGTAATTCAGGAAGACTGAAAGAATATGAT	3768
Db	1382	ACCATCATTCAGACAGTGCACAGATAATAGTTTTCAGTAATTCAGGAAGACTGAAAGAATATGAT	1441
QY	3769	GAGCGGTATGTTTGTCTGCAAAATAAGACAGCGCTATTTTACAGATGGTGCACAACTG	3828
Db	1442	GAGCGGTATGTTTGTCTGCAAAATAAGACAGCGCTATTTTACAGATGGTGCACAACTG	1501
QY	3829	GGCAAGCGCAAGCGCTGCGCTCTCACTGAAACAGCAAAACAGGCTATATCTTTCAAAAGAAAT	3888
Db	1502	GGCAAGCGCGAAGCGCTGCGCTCACCGAAACAGCAAAACAGGCTATATCTTTCAAGCGAAT	1561
QY	3889	TATCCACATATTTGTCATCATGACACCATGGTTTACAAACACATCTTCCAATGACAGCCCTCG	3948
Db	1562	TATCCACATATTTACATTTTACAGCGCGCGGTTATGAACACCTTCCAATGACAGCCCTCG	1621
QY	3949	ACCTTAACATTTTCGAGACGACACTGTGA	3978
Db	1622	GCCTTAACAATATTTGAACAGCATTTGTGA	1651
RESULT 6			
BM462073			
LOCUS	AGENCOURT_6424622 NIH_MGC_67 Homo sapiens cdna clone IMAGE:5491146	1084 bp	mRNA linear EST 05-FEB-2002
DEFINITION	5', mRNA sequence.		
ACCESSION	BM462073		
VERSION	BM462073.1	GI:18511113	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-x@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLNL12111 row: c column: 19 High quality sequence stop: 657.		
FEATURES	Location/Qualifiers		
source	1. .1084 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5491146" /tissue_type="retinoblastoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 67" /notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."		
ORIGIN			
Query Match	18.5%	Score 734;	DB 4; Length 1084;

Best Local Similarity 100.0%; Pred. No. 1.2e-197; Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	2003 CTTGAAAGATGGTCTCTGAGAGCCAAAGATACAGAAATGTCCTCCAGTACACTATCAG 2062
Db	1 CTTTGAAGATGGTCTCTGAGAGCCAAAGATACAGAAATGTCCTCCAGTACACTATCAG 60
Qy	2063 AGGAGAACGTTCTGAAGGAAAGTGGTTTTCAGGCTATAGAAATTAATCTCAGAGCTG 2122
Db	61 AGGAGAACGTTCTGAAGGAAAGTGGTTTTCAGGCTATAGAAATTAATCTCAGAGCTG 120
Qy	2123 GTGCTCACTGGATGCTCTCATTTTCCTTATTTCTCTTAACACCTGCAGCTCAGGTTCCCT 2182
Db	121 GTGCTCACTGGATGCTCTCATTTTCCTTATTTCTCTTAACACCTGCAGCTCAGGTTCCCT 180
Qy	2183 ATGTGCTTCAAGATGGTGGCTTTCATCTACTGGGCAACAAACAAAGATATGCTAAATGCA 2242
Db	181 ATGTGCTTCAAGATGGTGGCTTTCATCTACTGGGCAACAAACAAAGATATGCTAAATGCA 240
Qy	2243 CTGTAAATGGAGGAGGAAATGTACCCGAGAGCTAGATCTTAACCTGTACTTAGGAATTT 2302
Db	241 CTGTAAATGGAGGAGGAAATGTACCCGAGAGCTAGATCTTAACCTGTACTTAGGAATTT 300
Qy	2303 ATTCAGGTTTAACTGTAGTACCGTCTTTTGGCATAGCAAGATCTCTATTTGTTATTTCT 2362
Db	301 ATTCAGGTTTAACTGTAGTACCGTCTTTTGGCATAGCAAGATCTCTATTTGTTATTTCT 360
Qy	2363 ACGTCTTGTTAACTCTTCAAACTTTGCAACAAAAATGTTTGAAGTCAATTTCTGAAAG 2422
Db	361 ACGTCTTGTTAACTCTTCAAACTTTGCAACAAAAATGTTTGAAGTCAATTTCTGAAAG 420
Qy	2423 CTCGGTATTATTTCTTGATAGAAATCCATAGGAAGAAATTTAAATCGTTTCTCCAAAG 2482
Db	421 CTCGGTATTATTTCTTGATAGAAATCCATAGGAAGAAATTTAAATCGTTTCTCCAAAG 480
Qy	2483 ACATTGACACATTCGATGATTTGCTGCGCTGACGTTTATAGATTTTCATCCAGACATTGC 2542
Db	481 ACATTGACACATTCGATGATTTGCTGCGCTGACGTTTATAGATTTTCATCCAGACATTGC 540
Qy	2543 TACAAGTGGTGGTGGTCTCTGTGGCTGTGGCGGTGATTCCTTGGATCGCAATACCTT 2602
Db	541 TACAAGTGGTGGTGGTCTCTGTGGCTGTGGCGGTGATTCCTTGGATCGCAATACCTT 600
Qy	2603 TGGTCCCTTGGAAATCATTTTCAATTTTCTTCGGCGATATTTTTCGAAACGTCAGAG 2662
Db	601 TGGTCCCTTGGAAATCATTTTCAATTTTCTTCGGCGATATTTTTCGAAACGTCAGAG 660
Qy	2663 ATGTGAAGCGCTCGAATCTACAACTCGAGTCCAGTGTTCCTCCACTTTGTCTATCTCTC 2722
Db	661 ATGTGAAGCGCTCGAATCTACAACTCGAGTCCAGTGTTCCTCCACTTTGTCTATCTCTC 720
Qy	2723 TCCAGGGGCTCTGG 2736
Db	721 TCCAGGGGCTCTGG 734
RESULT 7 BP382967 LOCUS DEFINITION BP382967 Sugano cDNA library, ilea mucosa Homo sapiens cDNA clone kai1118, mRNA sequence. ACCESSION BP382967 VERSION BP382967.1 GI:52419393 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 915) Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions	

Genome Res. 14 (9), 1711-1718 (2004) Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp.	
FEATURES	Location/Qualifiers
	source
1..915 /organism="Homo sapiens" /mol_type="mrna" /db_xref="taxon:9606" /clone="kai1118" /tissue type="ilea mucosa" /clone_lib="Sugano cDNA library, ilea mucosa"	
ORIGIN	
Query Match 18.2%; Score 725; DB 5; Length 915; Best Local Similarity 98.0%; Pred. No. 4.2e-195; Matches 750; Conservative 0; Mismatches 7; Indels 2; Gaps 2;	
Qy	2221 AACCAAGTATGTAATGTCACCTGTAATGGAGGAGGAATGTAAACCGAGAGCTAGAT 2280
Db	1 AACCAAGTATGTAATGTCACCTGTAATGGAGGAGGAATGTAAACCGAGAGCTAGAT 60
Qy	2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATA 2340
Db	61 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGTACCGTCTCTTTTGGCATA 120
Qy	2341 GCAAGATCTCTATTTGGTATTTCTACGTCCTTGTAACTTTTCAAAAATTTTGCACAA 2400
Db	121 GCAAGATCTCTATTTGGTATTTCTACGTCCTTGTAACTTTTCAAAAATTTTGCACAA 180
Qy	2401 ATGTTTGAATCAATCTGAAGCTCCGGTATTTATTTCTTGATAGAAATCCAATAGGA 2460
Db	181 ATGTTTGAATCAATCTGAAGCTCCGGTATTTATTTCTTGATAGAAATCCAATAGGA 240
Qy	2461 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTTGTCCGCTGACGTTT 2520
Db	241 ATTTTAAATCGTTTCTCCAAAGACATTTGGACACTTTGGATGATTTTGTCCGCTGACGTTT 300
Qy	2521 TTAGATTTTCAACAGACATTTGTACAGTGGTGGTGGTGTCTCTGTGGCTGTGGCGGTG 2580
Db	301 TTAGATTTTCAACAGACATTTGTACAGTGGTGGTGGTGTCTCTGTGGCTGTGGCGGTG 360
Qy	2581 ATTCTTGGATCCCAATACCTTGGTCCCTTGGATCAATTTTCATTTTCTTCGGCGA 2640
Db	361 ATTCTTGGATCCCAATACCTTGGTCCCTTGGATCAATTTTTCATTTTCTTCGGCGA 420
Qy	2641 TATTTTGTGAAACGTCAGAGATGTGAAGCGCTGGAATCTCAACTCCGAGTCCAGTG 2700
Db	421 TATTTTGTGAAACGTCAGAGATGTGAAGCGCTGGAATCTCAACTCCGAGTCCAGTG 480
Qy	2701 TTTTCCCACTTGTCACTTCTCTCCAGGGGCTCTGGACCAATCCGGGCAATCAAAAGCAGAA 2760
Db	481 TTTTCCCACTTGTCACTTCTCTCCAGGGGCTCTGGACCAATCCGGGCAATCAAAAGCAGAA 540
Qy	2761 GAGAGTGTCCAGCACTGTTTGTATGCAACACAGATTTTACATTCAGAGGCTTGGTCTTG 2820
Db	541 NAGAGTGTCCAGCACTGTTTGTATGCAACACAGATTTTACATTCAGAGGCTTGGTCTTG 600
Qy	2821 TTTTGTGAAACGTCCTCGCTGGTTCGGCTCCGCTCTGGATGCCATCTGTGCCATGTTTGTG 2880
Db	601 TTTTGTGAAACGTCCTCGCTGGTTCGGCTCCGCTCTGGATGCCATCTGTGCCATGTTTGTG 660
Qy	2881 ATCATCGTCCCTTGGGTCCTGATTTCTGGCAAAAATCTCTGGATGCCGGGACAGTTGGT 2940
Db	661 -TCATCGTCCCTTGGGTCCTGATTTCTGGCAAAAATCTCTGGATGCCGGGACAGTTGGT 718
Qy	2941 TTGGCACTGTCTTATGCTCCCTCAGCTCATGGGATGTTT 2979
Db	719 TTGGCACTGTCTTATGCTCCCTCAGCTCATGGGATGTTT 757



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RESULT 8
CF597322      747 bp mRNA linear EST 26-SEP-2003
LOCUS
DEFINITION   AGENCOURT 15657890 NICHHD Hs Ov1 Homo sapiens cDNA clone
IMAGE:30705136 5', mRNA sequence.
CF597322
ACCESSION
VERSION      CF597322.1 GI:36354582
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 747)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gregory F. Erickson, Ph.D.
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM255 row: e column: 17
High quality sequence stop: 512.
FEATURES
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1..747
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30705136"
/tissue_type="Ovary"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NICHHD Hs Ov1"
/note="Vector: pBR-322; Site 1: SfiI (ggccattagcc);
Site 2: SfiI (ggcgctggcc); Library is oligo-dT primed
and directionally cloned. Granulosa lutein cells aspirated
from preovulatory follicles of normal cycling women
undergoing ovulation induction for infertility due to male
factor and normal donors. The cells were from follicles
stimulated with Lupron, FSH and hCG. 5' and 3' adaptors
were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 2.23
kb (range 1.0-4.5 kb). 14/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA)."
```

Query Match 18.0%; Score 717.4; DB 7; Length 747;  
Best Local Similarity 99.1%; Pred. No. 5.7e-193;  
Matches 732; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy 1057 GTGCGATGACGCTGTATGGGCTGTGCGGCTGACGTTACCTCTCTTCCCTCAGCC 1116
Db 4 GTGCGATGACGCTGTATGGGCTGTGCGGCTGACGTTACCTCTCTTCCCTCAGCC 63
Qy 1117 ATTGAGAGGTTGTCAGAGGCAATCGTCAGATCCGAGAGTCCAGACCTTTTGTCTACTT 1176
Db 64 ATTGAGAGGTTGTCAGAGGCAATCGTCAGATCCGAGAGTCCAGACCTTTTGTCTACTT 123
Qy 1177 GATGAGATATCACAGCGCAACCGTCAGCTGCCGTGACATGTTAAAGATGGTCATGTG 1236
Db 124 GATGAGATATCACAGCGCAACCGTCAGCTGCCGTGACATGTTAAAGATGGTCATGTG 183
Qy 1237 CAGGATTTTACTGCTTTTGGGATAAGGCATCAGAGACCCCACTCTACAGGCGCTTTCC 1296

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Db 184 CAGGATTTTACTGCTTTTGGGATAAGGCATCAGAGACCCCACTCTACAGGCGCTTTCC 243
Qy 1297 TTTACTGTACAGACCTGCGGAATTTAGCTGTGTGTCGCCCCCGTGGAGCAGGGAAGTCA 1356
Db 244 TTTACTGTACAGACCTGCGGAATTTAGCTGTGTGTCGCCCCCGTGGAGCAGGGAAGTCA 303
Qy 1357 TCACCTTTAAAGTGCCTGCTCGGGAAATTTGGCCCCCAAGTCACGGGCTGGTCAGCGTGCAT 1416
Db 304 TCACCTTTAAAGTGCCTGCTCGGGAAATTTGGCCCCCAAGTCACGGGCTGGTCAGCGTGCAT 363
Qy 1417 GGAAGAAATTCCTATGTCTCTCAGCAGCCCTGGGTGTCTTCGGGAACCTCTCAGGAGTAAT 1476
Db 364 GGAAGAAATTCCTATGTCTCTCAGCAGCCCTGGGTGTCTTCGGGAACCTCTCAGGAGTAAT 423
Qy 1477 ATTTTATTTGGGAAGAAATACGAAAGAACGATATGAAAAGTCATATAAGCTTTGTCT 1536
Db 424 ATTTTATTTGGGAAGAAATACGAAAGAACGATATGAAAAGTCATATAAGCTTTGTCT 483
Qy 1537 CTGAAAAGGATTTTACAGCTGTTGGAGGATGGTGTATCTGACTGTGATAGGAGATCGGGGA 1596
Db 484 CTGAAAAGGATTTTACAGCTGTTGGAGGATGGTGTATCTGACTGTGATAGGAGATCGGGGA 543
Qy 1597 ACCACGCTGAGTGGAGGCGGAGAACGACGGTAAACCTTCAAGAGCAGTGTATCAAGAT 1656
Db 544 ACCACGCTGAGTGGAGGCGGAGAACGACGGTAAACCTTCAAGAGCAGTGTATCAAGAT 603
Qy 1657 GCTGACATCTATCTCTGGAGCATCTCTCAGTCAGTAGATGGGGAAGTTAGCAGACAC 1716
Db 604 GCTGACATCTATCTCTGGAGCATCTCTCAGTCAGTAGATGGGGAAGTTAGCAGACAC 663
Qy 1717 TTGTTGCAACTGTGTATTTGTCAAAATTTGCATGAGAAGATCA-CAATTTTGTGACTCA 1775
Db 664 TTGTTGCAACTGTGTATTTGTCAAAATTTGCATGAGAAGATCAACCATTTTGTGACTCA 723
Qy 1776 TCAGTTGCACTACCTCAAA 1794
Db 724 TCCGTTGCACTACCTCAAA 742

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RESULT 9  
CD657554 797 bp mRNA linear EST 18-JUN-2003  
LOCUS  
DEFINITION AGENCOURT 14537985 NIA Human H1 Embryonic Stem Cell cDNA Library  
(Long) Homo sapiens cDNA clone IMAGE:30420491 5', mRNA sequence.  
CD657554  
ACCESSION  
VERSION CD657554.1 GI:31899898  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 797)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA  
cDNA Library Preparation: Yulan Piao and Minoru KO  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information  
can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM496 row: m column: 12  
High quality sequence stop: 686.  
FEATURES  
source  
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Location/Qualifiers  
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/clone\_lib="NIA Human H1 Embryonic Stem Cell cDNA Library (Long)"  
/notes=vector: pCMV-Sport6; Site.1: NotI; Site.2: SalI;  
This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199] from WA01 cell line. Undifferentiated human ES cell line WA01/H1 was obtained from Wicell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and BOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV  
(Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with Trizol Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID: 11544199] Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGCGCGCCTTTT-3'] from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

## ORIGIN

Query Match 17.9%; Score 712.8; DB 6; Length 797;  
Best Local Similarity 99.6%; Pred. No. 1.2e-191;  
Matches 725; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
Qy 892 CTTATTACCAATTGAGAAAGAGGATTCGAAGATTCGAGAAGTTCCTGCCTCAGG 951  
Db 11 CTTATTACCAATTGAGAAAGAGGATTCGAAGATTCGAGAAGTTCCTGCCTCAGA 70  
  
Qy 952 GGGATGAATTGGCTTCGTTTTTCAGTGCAGCAAAATCATCGTGTGTGACCTTCACC 1011  
Db 71 GGGATGAATTGGCTTCATTTTTTCAGTGCAGCAAAATCATCGTGTGTGACCTTCACC 130  
  
Qy 1012 ACCTACGTGCTCCTCGGAGTGTGATCACAGCCGCGGTGTCGTGGCAGTGACGCTG 1071  
Db 131 ACCTACGTGCTCCTCGGAGTGTGATCACAGCCGCGGTGTCGTGGCAGTGACGCTG 190  
  
Qy 1072 TATGGGCTGTGGGCTGACGGTTACCGTCTTCTTCCCTCAGCCATTGAGAGGGTGCA 1131  
Db 191 TATGGGCTGTGGGCTGACGGTTACCGTCTTCTTCCCTCAGCCATTGAGAGGGTGCA 250  
  
Qy 1132 GAGCAATCGTCAGCATCCGAAGAAATCCAGACCTTTTGTGCTACTTGATGATATACAG 1191  
Db 251 GAGCAATCGTCAGCATCCGAAGAAATCCAGACCTTTTGTGCTACTTGATGATATACAG 310  
  
Qy 1192 CGCAACCGTCAGCTGCCGTGATGGTAAAGATGGTGCATGTGCAAGGATTTTACTGCT 1251  
Db 311 CGCAACCGTCAGCTGCCGTGATGGTAAAGATGGTGCATGTGCAAGGATTTTACTGCT 370  
  
Qy 1252 TTTTGGGTAAGGATCAGAGACCCCACTACAAGCCCTTCTTACTGTGACACCT 1311  
Db 371 TTTTGGGTAAGGATCAGAGACCCCACTACAAGCCCTTCTTACTGTGACACCT 430  
  
Qy 1312 GGCGAATTGTTAGTGTGGTCGGCCCGTGGGAGCAGGGAAGTTCATCACTGTTAAGTGCC 1371

Db 431 GCGCAATTGTTAGCTGTGTGTCGCGCCCGTGGAGCAGGGAAGTCATCACTGTTAAGTGCC 490  
  
Qy 1372 GTGCTCGGGGAATTGGCCCCCAAGTCACGGCTGGTTCAGCGTGCATGGAAGAATTGCCAT 1431  
Db 491 GTGCTCGGGGAATTGGCCCCCAAGTCACGGCTGGTTCAGCGTGCATGGAAGAATTGCCAT 550  
  
Qy 1432 GTGCTCAGCAGCCCTGGGGTTCCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAG 1491  
Db 551 GTGCTCAGCAGCCCTGGGGTTCCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAG 610  
  
Qy 1492 AATATACAAAAGGAACGATATGAAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTA 1551  
Db 611 -AATACGAAAGGACGATATGAAAAAGTCATAAAGCTTGTGCTCTGAAAAAGGATTTA 669  
  
Qy 1552 CAGCTGTTGAGAGTGTGATCTGACCTGTGATAGGAGATCGGGGAACACCGCTGAGTGA 1611  
Db 670 CAGCTGTTGAGAGTGTGATCTGACCTGTGATAGGAGATCGGGGAACACCGCTGAGTGA 729  
  
Qy 1612 GGGCAGAA 1619  
Db 730 GGGCAGAA 737  
  
RESULT 10  
CR704782  
LOCUS CR704782 1679 bp mRNA linear HTC 19-AUG-2004  
DEFINITION Tetraodon nigroviridis full-length cDNA.  
ACCESSION CR704782  
VERSION CR704782.1 GI:51202691  
KEYWORDS HTC; cDNA; full-length; Tetraodon nigroviridis.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ruteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Tetraodon.  
REFERENCE 1 (bases 1 to 1679)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -  
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
The sequences are based on single pass reads.  
More information available at  
http://www.genoscope.cns.fr/tetraodon.  
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Best Local Similarity 68.6%; Pred. No. 7.2e-189;  
Matches 970; Conservative 0; Mismatches 444; Indels 0; Gaps 0;  
  
Qy 2480 AAGACATTTGACACTTGGATGATTTGCTGCGCTGACGTTTTTAGATTTTCATCCAGACAT 2539  
Db 33 AAGCAATTGGCAGTTGGAATCTTAAATGCCATGATTTTTGTGGATTTTATTCAGTTGT 92  
  
Qy 2540 TGCTACAAGTGGTGGTGTCTCTGTGGCTGTGGCGGTGATTCCTTGGATCCGCAATAC 2599  
Db 93 TCCTGCAAAATCCCTGGGCGGTGATTCGTGTGACGCTCAGTGATTCCTCGGATTTGATCC 152  
  
Qy 2600 CCTTGGTTCCTTGAATCATTTTCAATTTTCTTCGCGGATATTTTGGAAACGTCAC 2659  
Db 153 CTGTGCTTCCTCTTTCATCGTCTTCACTACCTTCCTGCTGTTTCTTCGACAGGCTCA 212  
  
Qy 2660 GAGATGGAAGCGCTCGGAATCTACAACTCGAGTCCAGTGTGTTCCCACTTGTCACTT 2719  
Db 213 GAGATGGAAGCGCTCGAGTCAACCACTCGAAGTCCCGTCTTCTCCCACTTGTCTCGT 272

QY 2720 CTCTCCAGGGCTCTGACACCATCCGGGCATACAAAGCAGAGAGAGGTGTTCAGGAACCTGT 2779  
 Db |||||  
 QY 273 CTCTTCAGGGCTGTGGACCATCCGAGCATTCAGGCGAGAGGACAGGTTCCAGAAAGCCT 332  
 Db |||||  
 QY 2780 TTGATGACACACAGGATTTACATTCAGAGGCTTGGTCTTGTTGTTTTCAGAAAGTCCCGCT 2839  
 Db |||||  
 QY 333 TTGATGAATATCAAGACTTGCACTCACAAGCGCTGGTCTCTGTTCTGACAAATCTCGCT 392  
 Db |||||  
 QY 2840 GTTTCGGCTCGCTGTCGATCTGTCATGTTGTTGTCATCATCTGTTGCTTCGGT 2899  
 Db |||||  
 QY 393 GTTTGTCTTCTGCTCGATGCCATCTGTTCCGCTCTTGTAAACGCTCACTACATTTGCT 452  
 Db |||||  
 QY 2900 CCTGTATTGGCAAAAACCTCTGATGCCGGGCGAGGTTGGTTTGGCACTGTCTTATGCC 2959  
 Db |||||  
 QY 453 GCCTGTCTCAGAAACACAGCTGATCGAGCTCTGTGGTCTGCTGTGACCTACGCT 512  
 Db |||||  
 QY 2960 TCAGCTCATGGGATGTTTCAGTGGTGTGTTTCGACAAAGTGTGAAGTTGAGAAATGA 3019  
 Db |||||  
 QY 513 CTACGTTGATGGGAATGTTCCAGTGGCTGTGACACAGAGTGCAGAAAGTAGAGAACTTGA 572  
 Db |||||  
 QY 3020 TGATCTCAGTAGAAGGCTCAATGAATACACAGACCTTGAAGAGAGGATGAATCTTTGACAAATGTA 3079  
 Db |||||  
 QY 573 TGAGCTCAGTGGAGGATGTTGATGATCACTGAGCTGGAGAGTGAAGCACCATGGGAAA 632  
 Db |||||  
 QY 3080 ATCAGAAACGCCACCCAGCCTGGGCCCATGAAGAGGAGTGAATCTTTGACAAATGTA 3139  
 Db |||||  
 QY 633 CCCAAAACGCTCTCCACCGATGGCTAGTAAAGGCTTGGTACCTTTGACCGTGTCA 692  
 Db |||||  
 QY 3140 ACTTCATGTACAGTCCAGTGGGCTCTGGTACTGAAGACATCTGACAGCACTCAATTAAT 3199  
 Db |||||  
 QY 693 GCTTCTCTACAGTGAATAAGCCGCGGTCTCCACAGCTTGAAGCCATGTTTCTAC 752  
 Db |||||  
 QY 3200 CACAAGAAAGGTTGGCATTGTGGAGAACCGGAGCTGGAAGTTCCTCATCTCAG 3259  
 Db |||||  
 QY 753 CTCAGAAAGGTTGGCATTGTGGGTGCGACCGGTCTGGAAGAGTCTCTGGTCTCCG 812  
 Db |||||  
 QY 3260 CCCTTTTGTAGATTGTGAGAACCCCAAGCTAAAATTTGGATTGTGAAGATCTTGACAACTG 3319  
 Db |||||  
 QY 813 CGCTGTTCCGATTGGCAGAGCCTCAGGGAATAATCTACATCGATGGGCTTCTCAGCTCAG 872  
 Db |||||  
 QY 3320 AAATTGACTTCAGATTGAAGGAAGAAATGTCAATCACTCACTCAGGAACCTGTTTTGT 3379  
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 QY 873 AGATCGGTCTCTCAGATTGCGCCAGAGATGTCCATATATACCTCAGGACCCAGTGTGT 932  
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 QY 933 TTACAGGTCATGAGGAAGAACCTGATCTCTTTTAAACCAACACACAGACGAGGAACCTGT 992  
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 QY 3440 GGAATGCTTACAGAGGTCAACTTAAAGAAACCATTTGAAGATCTTCTGTTAAATGG 3499  
 Db |||||  
 QY 993 GGAAGCTCTGGAGAGGTGACGTGAAGTCACTGTTGGAGGACCTCCGGGAGCTGG 1052  
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 QY 3500 ATACTGAATTAGCAAGATCAGGATCCAAATTTAGTGTGGCAAGACAACTGTGTGCC 3559  
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 QY 1053 AGACGGTGTGGCGAGTCCGGCTCCAACTTACGCTGGGCGAGACAGCTGTGTGTC 1112  
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 QY 3560 TTGCCAGGCAATCTCAGGAAATCAGATATTGATTTGATGAAGCAGCAGCAATG 3619  
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 QY 3620 TGATCCAGAACTGATGAGTTAATACAAAATAAATAATCCGGAGAAATTTGCCCACTGCA 3679  
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 Db |||||  
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 QY 1293 TTGATGAGGAAACATACATGTCATTCAGCGACCGGTTTCACTACTCTCAAGATCCCATG 1352  
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QY 3800 GCCTATTTTCAAGATGGTGCACAACTGGCAAGCAGAGAGCGCTCCCTCACTGAAA 3859  
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 Db |||||  
 QY 3860 CAGCAAAACAGGTATACCTTCAAAAGAAATATATCC 3893  
 Db |||||  
 QY 1413 CGTCTAAAGAGGCGTACAGCGGTGGAGTCCATCC 1446  
 Db |||||  
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 DEFINITION AGENCOURT 15990281 NIH MGC 221 Homo sapiens cDNA clone  
 IMAGE:30708953 5', mRNA sequence.  
 CF786044  
 ACCESSION CF786044.1 GI:37751656  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 810)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cga@nci.nih.gov  
 Tissue Procurement: James Martin, University of Iowa  
 cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDAM1075 row: p column: 18  
 High quality sequence stop: 579.  
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 /lab\_host="DH10B Tona"  
 /clone\_lib="NIH\_MGC\_221"  
 /notes="Organ: mixed; Vector: pYX-Asc; Site 1: EcoRI;  
 Site 2: NotI; Library is oligo-dT primed and directionally  
 cloned. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated with  
 EcoR I adaptor, digested with Not I and then cloned  
 directionally into pYX-Asc vector. Average insert size  
 4-5kb. Adaptors 5'(AATTCGGCAGG)3' and 5'd  
 (CCTCTCGCG)3'. 3' Linker sequence - GCGGCGCTCAGAGCC T18.  
 Sequencing primers 3'end: T3 promoter primer 5'd  
 (ATTAACTCTCACTAAGGA)3'. 5' End: T7 promoter primer 5'd  
 (TAATACGACTCATAGG)3'. Library was constructed in the  
 laboratory of M. Bento Soares. Note: this is a NIH\_MGC  
 Library"

ORIGIN

Query Match 16.7%; Score 665.6; DB 7; Length 810;  
 Best Local Similarity 97.2%; Pred. No. 3.9e-178;  
 Matches 688; Conservative 0; Mismatches 19; Indels 1; Gaps 1;  
 QY 923 CCAAGATTCGAGAGTTCCTGCTCAGGGGGATGAATTTGGCTTCCTTTTTCAGTGCAA 982  
 Db 8 CCAAGATTCGAGAGTTCCTGCTCAGGGGGATGAATTTGGCTTCCTTTTTCAGTGCAA 67  
 QY 983 GCAAAATCATCGTGTGTTGTGACCTTACCACCTACGTGCTCTCGGAGGTGTGATCAG 1042

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Db      68  GCAAAATCATCGTGTGTTGTGACCTTACACACCTACGTCCTCGGCAGTGTGATCACAG 127
Qy      1043  CGAGCCGCGTGTGCGTGGCAGTGCAGCTGTATGGGGCTGTGCGGCTGACGGTTACCCCTCT 1102
Db      128  CGAGCCGCGTGTGCGTGGCAGTGCAGCTGTATGGGGCTGTGCGGCTGACGGTTACCCCTCT 187
Qy      1103  TCTTCCCTCAGCCATTGAGGGGTGTCAGAGGCAATCGTCAGCATCCGAGGATCCAGA 1162
Db      188  TCTTCCCTCAGCCATTGAGGGGTGTCAGAGGCAATCGTCAGCATCCGAGGATCCAGA 247
Qy      1163  CTTTCTTGTCTACTGATGAGATATCAGCGCAGCTGAGCTGCGCTCAGATGGTAAAA 1222
Db      248  CTTTCTTGTCTACTGATGAGATATCAGCGCAGCTGAGCTGCGCTCAGATGGTAAAA 307
Qy      1223  AGATGTCATGTCAGGATTTTACTCTCTTTTGGGATAAGGCATCAGACCCCACTC 1282
Db      308  AGATGTCATGTCAGGATTTTACTCTCTTTTGGGATAAGGCATCAGACCCCACTC 367
Qy      1283  TACAGGCCCTTCTTACTGTCAGACTGCGGCAATTTGTTAGCTGTGTCGGCCCGTGG 1342
Db      368  TACAAGGCCCTTCTTACTGTCAGACTGCGGCAATTTGTTAGCTGTGTCGGCCCGTGG 427
Qy      1343  GAGCAGGGAAGTCACTGTTAAGTCCCTGCTCGGGGAATTGGCCCCCAAGTCACGGGC 1402
Db      428  GAGCAGGGAAGTCACTGTTAAGTCCCTGCTCGGGGAATTGGCCCCCAAGTCACGGGC 487
Qy      1403  TGTGTCAGCGTCATGGAAGATTTGCTGTCAGAGCCCTGGGTGTTCTCGGGAA 1462
Db      488  TGGTCAGCGTCATGGAAGATTTGCTGTCAGAGCCCTGGGTGTTCTCGGGAA 547
Qy      1463  CTCGAGGAGTAAATTTTATTTTGGGAAGAAATACGAAAGGACGATATGAAAAGTCA 1522
Db      548  CTCGAGGAGTAAATTTTATTTTGGGAAGAAATACGAAAGGACGATATGAAAAGTAA 607
Qy      1523  TAAAGGCTTGCTCTGAAAAGGATTTACAGCTGTTTGGAGGATGGTGATCTGACTGTGA 1582
Db      608  TATAAGCTTGCTCTGAAAAGGA-TTACAGCTGTTTGGAGGATTTGATCTGACTGTGA 666
Qy      1583  TAGGAGATCGGGGAACCACTGAGTGGAGGGCGAGAAAGCACGGGTAA 1630
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RESULT 12
LOCUS   BUI186494
DEFINITION 7936979 NIH_MGC_92 Homo sapiens cdna clone IMAGE:6012768
          5', mRNA sequence.
ACCESSION BUI186494
VERSION   BUI186494.1 GI:22700478
KEYWORDS  EST.
SOURCE    Homo sapiens (human)

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ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 951)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: csapbs@remail.nih.gov
          Tissue Procurement: ARCC
          CDNA Library Preparation: Life Technologies, Inc.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAMI3204 row: j column: 01
          High quality sequence stop: 539.
          Location/Qualifiers
            1. .951
          SOURCE

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/clone="IMAGE:6012768"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/notes="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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Query Match	Best Local Similarity	Score	DB 5;	Length	951;
Matches	723;	Conservative	0;	Mismatches	13;
				Indels	5;
				Gaps	5;
Qy	219	TGACGCACAGAACCTTCTTTTAAAGAGCAATCATAAAGTGTACTTGGAAATCTTATTT	278		
Db	1	TGACGCACAGAACCTTCTTTTAAAGAGCAATCATAAAGTGTACTTGGAAATCTTATTT	60		
Qy	279	AGTTTGGGAAATTTTACGTTAAATGAGGAAAGTGCACAAAGTAATCCAGCCCATATTTT	337		
Db	61	AGTTTGGGAAATTTTACGTTAAATGAGGAAAGTGCACAAAGTAATCCAGCCCATATTTT	120		
Qy	338	TGGGAAATTAATTAATTTTGAATAATATGATCCATGGATTCGTGGCTTTGAACA	397		
Db	121	TGGGAAATTAATTAATTTTGAATAATATGATCCATGGATTCGTGGCTTTGAACA	180		
Qy	398	CAGCTACGCGTATGCCAGCGTCTGACTTTTGGACGCTCATTTTGGCTTACTGTCATC	457		
Db	181	CAGCTACGCGTATGCCAGCGTCTGACTTTTGGACGCTCATTTTGGCTTACTGTCATC	240		
Qy	458	ACTTATATTTTATCAGCTTCTGCTCGGATGAGTTACAGTACGATAGCCATATTTT	517		
Db	241	ACTTATATTTTATCAGCTTCTGCTCGGATGAGTTACAGTACGATAGCCATATTTT	300		
Qy	518	TGATTTATCGGAGGCACTTCGTCTTAGTAAACATGGCCATGGGAGAGCAACACAGGCC	577		
Db	301	TGATTTATCGGAGGCACTTCGTCTTAGTAAACATGGCCATGGGAGAGCAACACAGGCC	360		
Qy	578	AGATAGTCAATCTGCTGTCCAATGATGTAACAAGTTTGTATCAGGTGACAGTGTCTTAC	637		
Db	361	AGATAGTCAATCTGCTGTCCAATGATGTAACAAGTTTGTATCAGGTGACAGTGTCTTAC	420		
Qy	638	ACTTCTGTGGGAGGACCACTGCGAGCGATCGCAGTACTGCCCTTACTCTGGATGGAGA	697		
Db	421	ACTTCTGTGGGAGGACCACTGCGAGCGATCGCAGTACTGCCCTTACTCTGGATGGAGA	480		
Qy	698	TAGGAATATCGTGGCTGTGGGATGGCAGTCTTAATCATCTCTGCGCCCTGCAAGCT	757		
Db	481	TAGGAATATCGTGGCTGTGGGATGGCAGTCTTAATCATCTCTGCGCCCTGCAAGCT	540		
Qy	758	GTTTTGGGAAAGTTGTTCTCATCTAGGAGT-AAAACTGCAACTTTTCAAGGATCCAGG	816		
Db	541	GTTTTGGGAAAGTTGTTCTCATCTAGGAGTAAATACTGCACTTTTCAAGGATCCAGG	600		
Qy	817	ATCAGGACCAATGAATGAAGTTATACTGGTATTAAGGATATAATAAATGTAGCCT-GGGA	875		
Db	601	ATCAGGACCAATGAATGAAGTTATACTGGGATAAGGATATAATAAATGTAGCCTGGGA	660		
Qy	876	AAAGTCAATTTTCAATCTTATTACCA-TTTGAGAAAGAGGAGA-TTTCACAGATCTG	933		
Db	661	AAAGTCAATTTTCAATCTTATTACCAATTTTGAGAAAGAGGAGATTTTCCAGATCTG	720		
Qy	934	AGAAAGTTCCTGCTCAGGGG 954			
Db	721	AAAAAGTTCCTGCTCAGGGG 741			

RESULT 13  
BE879353

LOCUS BE879353 682 bp mRNA linear EST 20-OCT-2000  
DEFINITION 601484613F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3887306 5',  
mRNA sequence.  
ACCESSION BE879353  
VERSION BE879353.1 GI:10328129  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 682)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM9665 row: i column: 03  
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."  
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Query Match 16.0%; Score 638; DB 2; Length 682;  
Best Local Similarity 99.4%; Pred. No. 2.8e-170;  
Matches 682; Conservative 0; Mismatches 0; Indels 4; Gaps 4;  
QY 1286 AAGCCCTTTCTTACTGTGACACTGGCGAATTGTAGCTGTGGTGGCCCGCTGGAG 1345  
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QY 1346 CAGGGAAGTCATCACTGTTAAGTCCCGTCTCGGGGAATTGGCCCCAAGTCACGGGCTGG 1405  
DB 61 CAGGGAAGTCATCACTGTTAAGTCCCGTCTCGGGGAATTGGCCCCAAGTCACGGGCTGG 120  
QY 1406 TCACGCTGCATGGAAGATTGCCTATGTCTCAGCAGCCCTGGTGTCTCGGGAATC 1465  
DB 121 TCACGCTGCATGGAAGATTGCCTATGTCTCAGCAGCCCTGGTGTCTCGGGAATC 180  
QY 1466 TGAGGAGTAAATATTTTATTTGGGAAGAAATACGAAAGGACGATATGAAAAAGTCATAA 1525  
DB 181 TGAGGAGTAAATATTTTATTTGGGAAGAAATACGAAAGGACGATATGAAAAAGTCATAA 240  
QY 1526 AGGCTTGTGCTCTGAAAAAGATTATACAGCTGTGTGGAGGATGGTGTCTGACTGTGATAG 1585  
DB 241 AGGCTTGTGCTCTGAAAAAGATTATACAGCTGTGTGGAGGATGGTGTCTGACTGTGATAG 300  
QY 1586 GAGATCGGGGAACACCGCTGAGTGGAGGCGAAGAACGACGCGGTAAACCTTGCAGAGCAG 1645  
DB 301 GAGATCGGGGAACACCGCTGAGTGGAGGCGAAGAACGACGCGGTAAACCTTGCAGAGCAG 360  
QY 1646 TGTATCAAGATGTCGATCTATCTCTCTGGACGATCTCTCTCAGTGCAGTATGATCGGAG 1705  
DB 361 TGTATCAAGATGTCGATCTATCTCTCTGGACGATCTCTCTCAGTGCAGTATGATCGGAG 420  
QY 1706 TTAGCAGACACTTTGTCGAACCTGTGTATTGTCAAATTTTGTGATGAGAAGATCACAATTT 1765

DB 421 TTAGCAGACACTTTGTCGAACCTGTGTATTGTCAAATTTTGCATGAGAAGATCACAATTT 480  
QY 1766 TAGTGACTCATCTCAGTTCAGTACCTCAAGCTCAAGTCAAGTCTGATATTTGAAAGATG 1825  
DB 481 TAGTGACTCATCTCAGTTCAGTACCTCAAGCTCAAGTCAAGTCTGATATTTGAAAGATG 540  
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DB 541 GTAAATGGTGCAGAGGGGACTTTACACTGAGTTCTCTAAATCTGGTATAGATTTTGCT 600  
QY 1886 CCCTTTTAAAGAGGATTAAGAGGAAGTGAACACCTCCAGTTCAGGAACTCCACAC 1945  
DB 601 CCCTTTTAAAGAGGAT-ATGAGGAAAGTGAACAA-CTCCAGTTCAGGAACTCCACAC- 657  
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LOCUS 17000600043591 GRN\_PRENU Homo sapiens cDNA 5', mRNA sequence.  
DEFINITION CN410192  
ACCESSION CN410192  
VERSION CN410192.1 GI:47397316  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 639)  
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.  
TRANSCRIPTOME CHARACTERIZATION elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
CONTACT: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
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/db\_xref="taxon:9606"  
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/note="Oligo dt primed, full-length enriched cDNA library  
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conditions. Embryoid bodies were generated in the presence  
of all-trans retinoic acid and mitogens."  
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QY 3405 GGATCCCTTTAATGAGCAGCGATGAGGAACCTGTGGAATGCCTTACAAGAGGTACAACT 3464  
DB 61 GGATCCCTTTAATGAGCAGCGATGAGGAACCTGTGGAATGCCTTACAAGAGGTACAACT 120  
QY 3465 TAAAGAAACCAATGAAGATCTTCTGTTGTAATAATGATACTGAATTAGCAGATCAGGATC 3524

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Db 121 TAAAGAAACCATGAAAGATCTTCTGTAATAAGTACTGAATTAGCAGATCAGGATC 180
Qy 3525 CAATTTAGTGTGGACAAGACAACATGGTGTGCTTGGCCAGGCAATTCACGAAAAA 3584
Db 181 CAATTTAGTGTGGACAAGACAACATGGTGTGCTTGGCCAGGCAATTCACGAAAAA 240
Qy 3585 TCAGATATTGATTTATGATGAAGCGCGGCAAAATGTGGATCCAGAACTGATGATTAAT 3644
Db 241 TCAGATATTGATTTATGATGAAGCGCGGCAAAATGTGGATCCAGAACTGATGATTAAT 300
Qy 3645 ACAAAAAAATCCGGGAGAAATTTGCCCACTGCACCGTGTACCACTTGCACACAGATT 3704
Db 301 ACAAAAAAATCCGGGAGAAATTTGCCCACTGCACCGTGTACCACTTGCACACAGATT 360
Qy 3705 GAACACCAATTATTGACAGCGACAAGATAATGGTTTTTATAGATTCAGGAAGACTGAAAGAATA 3764
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Qy 3825 ACTGGCAAGCGAGAACCGCTGCCCTCACTGAAACAGCAAAACAGGTATATCTCAAAG 3884
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Qy 3945 CTCGACCTTAACATTTTTCGAGACAGCACTGTGA 3978
Db 601 CTCGACCTTAACATTTTTCGAGACAGCACTGTGA 634
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RESULT 15
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LOCUS CK776984 865 bp mRNA linear EST 20-FEB-2004
DEFINITION 966272 MARC 3BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CK776984
VERSION CK776984.1 GI:42731404
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 865)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Caeas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keefe,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: 95 row: B column: 8
Seq primer: GTAATACGACTCATATAGGG.
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Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
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Query Match 15.6%; Score 620.4; DB 7; Length 865;
Best Local Similarity 83.0%; Pred. No. 3.4e-165;
Matches 719; Conservative 0; Mismatches 146; Indels 1; Gaps 1;
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GenCore version 5.1.6  
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SUMMARIES

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1	500	12.6	500	6	AX046490 Sequence
2	366	9.2	486	6	A64694 Sequence 60
3	366	9.2	486	9	U83660 Human multi
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C 5	336	7.7	407	6	CQ508484 Sequence
6	283	7.1	442	6	CQ492361 Sequence
7	260	6.5	443	6	AR562517 Sequence
8	252	6.3	425	6	CQ510062 Sequence
9	250	6.3	250	6	AX046491 Sequence
10	216	5.4	291	6	AR400536 Sequence
11	216	5.4	291	6	AR403803 Sequence
12	216	5.4	291	6	AR564183 Sequence
13	216	5.4	291	6	AX201050 Sequence
14	216	5.4	291	6	AX267849 Sequence
15	211	5.3	439	6	BD076840 5' EST of
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C 22	176	4.4	412	6	CQ499514 Sequence
C 23	145	3.6	273	6	CQ506527 Sequence
24	142	3.6	329	6	CQ500896 Sequence
25	142	3.6	416	6	CQ479724 Sequence
C 26	141	3.5	409	6	CQ479541 Sequence
C 27	141	3.5	433	6	CQ500713 Sequence
C 28	141	3.5	433	6	CQ509639 Sequence
29	138	3.5	469	6	CQ488969 Sequence
30	138	3.5	469	6	CQ489729 Sequence
31	138	3.5	469	6	CQ495571 Sequence
32	137	3.4	350	6	CQ481131 Sequence
33	137	3.4	425	6	CQ471963 Sequence
C 34	136	3.4	462	6	CQ470313 Sequence
C 35	136	3.4	484	6	CQ479481 Sequence
C 36	133	3.3	372	6	CQ470373 Sequence
37	132	3.3	403	6	CQ479964 Sequence
38	132	3.3	422	6	CQ501136 Sequence
39	127	3.2	391	6	CQ474753 Sequence
C 40	125	3.1	363	6	CQ474681 Sequence
C 41	125	3.1	439	6	CQ504659 Sequence
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45	105	2.6	220	6	CQ474785 Sequence

ALIGNMENTS

RESULT 1  
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LOCUS AX046490 500 bp DNA linear PAT 24-NOV-2000  
DEFINITION Sequence 27 from Patent WO0058471.  
ACCESSION AX046490  
VERSION AX046490.1 GI:11344437  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Schuetz, J. and Fridland, A.  
TITLE Multidrug resistance associated proteins and uses thereof  
JOURNAL Patent: WO 0058471-A 27 05-OCT-2000;  
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)  
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RESULT 2
LOCUS A64694 486 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 60 from Patent WO9731111.
ACCESSION A64694
VERSION A64694.1 GI:4530759
KEYWORDS .
SOURCE .
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Oude, E.R., Paulusma, C.C., Bosma, P.J., Borst, P., Evers, R., Kool and Marcel.
TITLE A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM
JOURNAL Patent: WO 9731111-A 60 28-AUG-1997;
COMMENT INTRIGENE BV (NL)
Other publication AU 1736697 19970910.
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Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
LOCUS HSU83660 486 bp mRNA linear PRI 02-OCT-1997
DEFINITION Human multidrug resistance-associated protein homolog (MRP4) mRNA, partial cds.
ACCESSION U83660
VERSION U83660.1 GI:2439971
KEYWORDS .
SOURCE .
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS Kool, M., de Haas, M., Scheffer, G.L., Scheper, R.J., van Eijk, M.J., Juijn, J.A., Baas, F. and Borst, P.
TITLE Analysis of expression of cMOAT (MRP2), MRP3, MRP4, and MRP5, homologues of the multidrug resistance-associated protein gene (MRP1), in human cancer cell lines
JOURNAL Cancer Res. 57 (16), 3537-3547 (1997)
MEDLINE 97413640
PUBMED 9270026
REFERENCE 2 (bases 1 to 486)
AUTHORS Kool, M., de Haas, M., Pomme, N.J., Baas, F. and Borst, P.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-1997) Molecular Biology, Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
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Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
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 LOCUS  
 DEFINITION Sequence 40646 from Patent WO0160860.  
 ACCESSION CQ508779  
 VERSION CQ508779.1 GI:41475043  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Schlegel R., Endege, W.O. and Monahan, J.E.  
 TITLE Genes differentially expressed in human prostate cancer and their use  
 JOURNAL Patent: WO 0160860-A 40646 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)  
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LOCUS  
 DEFINITION Sequence 40351 from Patent WO0160860.  
 ACCESSION CQ508484  
 VERSION CQ508484.1 GI:41474748  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Schlegel R., Endege, W.O. and Monahan, J.E.  
 TITLE Genes differentially expressed in human prostate cancer and their use  
 JOURNAL Patent: WO 0160860-A 40351 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)  
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 Db 74 GAGGAAT 67

RESULT 6  
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 LOCUS  
 DEFINITION Sequence 24228 from Patent WO0160860.  
 ACCESSION CQ492361  
 VERSION CQ492361.1 GI:41457980  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Schlegel R., Endege, W.O. and Monahan, J.E.  
 TITLE Genes differentially expressed in human prostate cancer and their use  
 JOURNAL Patent: WO 0160860-A 24228 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)  
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Dd	127	TATGTTTTTGCTGC AAAATAAAGAGAGCGCTATTTTTACAAGATGGTGCAACACTGGGCAAG	186								
Qy	3835	GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAAACAG	3870								
Dd	187	GCAGAGCCCGCTGCCCTCACTGAAACAGCAAAAACAG	222								

RESULT	12
LOCUS	AR564183 Sequence 823 from patent US 6759515.
DEFINITION	291 bp DNA linear PAT 08-OCT-2004
ACCESSION	AR564183
VERSION	AR564183.1 GI:53979234
KEYWORDS	.
SOURCE	Unknown. Unclassified.
ORGANISM	1 (bases 1 to 291)
REFERENCE	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE	Compositions and Methods for the therapy and diagnosis of prostate cancer
JOURNAL	Patent: US 6759515-A 823 06-JUL-2004;
FEATURES	Location/Qualifiers . . .291 /organism="unknown" /mol_type="genomic DNA"
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RESULT 13
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LOCUS
DEFINITION Sequence 680 from Patent WO0151633.
ACCESSION AX201050
VERSION AX201050.1 GI:15390858
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 680 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
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/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3715 ATTCACAGCGCAAGAATAATGGTTTTAGATTTCAGAAAGACTGGAAGAATATGATGAGCCG 3774
Db 67 ATTCACAGCGCAAGAATAATGGTTTTAGATTTCAGAAAGACTGGAAGAATATGATGAGCCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACAACTGGGCAAG 3834
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Qy 3835 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 3870
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RESULT 14
AX267849 291 bp DNA linear PAT 26-OCT-2001
LOCUS
DEFINITION Sequence 823 from Patent WO0173032.
ACCESSION AX267849
VERSION AX267849.1 GI:16516495
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 680 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..291
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 5.4%; Score 216; DB 6; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACCTTTGCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGGAGAAATTTGCCACTGCACCGTGTAAACCTTTGCACACAGATTGAACACCAATT 66

Qy 3715 ATTCACAGCGCAAGAATAATGGTTTTAGATTTCAGAAAGACTGGAAGAATATGATGAGCCG 3774
Db 67 ATTCACAGCGCAAGAATAATGGTTTTAGATTTCAGAAAGACTGGAAGAATATGATGAGCCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACAACTGGGCAAG 3834
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACAACTGGGCAAG 186

Qy 3835 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 3870
Db 187 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 222
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REFERENCE
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hegler, W.T.
and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 823 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..291
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 67 ATTCACAGCGCAAGAATAATGGTTTTAGATTTCAGAAAGACTGGAAGAATATGATGAGCCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACAACTGGGCAAG 3834
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACAACTGGGCAAG 186

Qy 3835 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 3870
Db 187 GCAGAAGCCGCTGCCCTCCTCAGTGAACAGCAAAACAG 222

RESULT 15
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LOCUS
DEFINITION 5' EST of secretory protein expressed in prostate.
ACCESSION BD076840
VERSION BD076840.1 GI:22622443
KEYWORDS JP 2001512013-A/87.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 439)
AUTHORS Edwards, J.B.D.M., Duclert, A. and Lacroix, B.
TITLE 5' EST of secretory protein expressed in prostate
JOURNAL Patent: JP 2001512013-A 87 21-AUG-2001;
GENSET
OS Homo sapiens (human)
PN JP 2001512013-A/87
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505291
PR 01-AUG-1997 US 08/905144
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLERT, BRUNO PI
LACROIX
PC C12N15/09,C07K14/47,C12P21/02,C12Q1/02,C12Q1/68,C12N15/00 CC
Von Heijne matrix
CC score 6
CC seq IVFIIFILLLNTAA/QV
CC n=a, g, c or t Location/Qualifiers
FH Key 200..361
FT sig_peptide 226.
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Qy 2100 CTATAAGAAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCCT 2159
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Db 289 CTATAAGAAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCCT 348
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Qy 2160 AACACTGCAGCTCAGGTTGCCTATGTCTTCAAGATTGGTGGCTTTCATATACTGGGCAA 2219
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Db 349 AACACTGCAGCTCAGGTTGCCTATGTCTTCAAGATTGGTGGCTTTCATATACTGGGCAA 408
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Qy 2220 CAAACAAAGTATGCTAAATGTCACTGTAAAT 2250
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Db 409 CAAACAAAGTATGCTAAATGTCACTGTAAAT 439
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Copyright (c) 1993 - 2005 Compugen Ltd.

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- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	308	7.7	407	18	US-10-357-930-40351
C 3	283	7.1	442	18	US-10-357-930-24228
4	252	6.3	425	18	US-10-357-930-41929
5	216	5.4	291	9	US-09-759-143-823
6	216	5.4	291	9	US-09-780-669-823
7	216	5.4	291	9	US-09-822-827-823
8	216	5.4	291	9	US-09-895-793-823
9	216	5.4	291	9	US-09-895-814-823
10	216	5.4	291	13	US-10-012-896-823
11	216	5.4	291	16	US-10-144-678A-823

Sequence 823, App  
Sequence 41689, A  
Sequence 32647, A  
Sequence 11475, A  
Sequence 21416, A  
Sequence 27257, A  
Sequence 10183, A  
Sequence 31381, A  
Sequence 38394, A  
Sequence 32763, A  
Sequence 11591, A  
Sequence 11408, A  
Sequence 32580, A  
Sequence 41506, A  
Sequence 20836, A  
Sequence 21596, A  
Sequence 27438, A  
Sequence 12998, A  
Sequence 3829, Ap  
Sequence 2179, Ap  
Sequence 11348, A  
Sequence 2239, Ap  
Sequence 11831, A  
Sequence 33003, A  
Sequence 6620, Ap  
Sequence 6548, Ap  
Sequence 36526, A  
Sequence 36627, A  
Sequence 37078, A  
Sequence 36596, A  
Sequence 6652, Ap  
Sequence 2306, Ap  
Sequence 37040, A  
Sequence 2494, Ap

# ALIGNMENTS

RESULT 1  
US-10-357-930-40646/c  
; Sequence 40646, Application US/10357930  
; Publication No. US20040259086A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Endegge, Wilson  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10/357,930  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276  
; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/211,314  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/219,007  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/255,281  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 62232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40646  
; LENGTH: 424  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-357-930-40646

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 Db 321 CTGTCCAAATGATGTAACAAGTTTATCAGTGCAGTGTCTTACACTTCTCTGTGGGCA 262  
 Qy 652 GGACCACTGCAGGCGATCGGAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 711  
 Db 261 GGACCACTGCAGGCGATCGGAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 202  
 Qy 712 CTGTGCGGATGGCAGTGTCTTAATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 771  
 Db 201 CTGTGCGGATGGCAGTGTCTTAATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 142  
 Qy 772 TTCTCATCTCAGGAGTAAACTGCACTTTTACGGATGCCAGATGCCAGATGCCAGATGCC 831  
 Db 141 TTCTCATCTCAGGAGTAAACTGCACTTTTACGGATGCCAGATGCCAGATGCCAGATGCC 82  
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 Db 81 GAAGTTAATCTGGTATGAAGATTAATAAATGTATG 46

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US-10-357-930-40351/c  
 ; Sequence 40351, Application US/10357930  
 ; Publication No. US20040259086A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlegel, Robert  
 ; APPLICANT: Endege, Wilson  
 ; APPLICANT: Monahan, John  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER  
 ; FILE REFERENCE: MRI-007BCN  
 ; CURRENT APPLICATION NUMBER: US/10/357,930  
 ; CURRENT FILING DATE: 2003-02-04  
 ; PRIOR APPLICATION NUMBER: 09/785,276  
 ; PRIOR FILING DATE: 2003-02-16  
 ; PRIOR APPLICATION NUMBER: 60/183,319  
 ; PRIOR FILING DATE: 2000-02-17  
 ; PRIOR APPLICATION NUMBER: 60/189,862  
 ; PRIOR FILING DATE: 2000-03-16  
 ; PRIOR APPLICATION NUMBER: 60/207,454  
 ; PRIOR FILING DATE: 2000-05-25  
 ; PRIOR APPLICATION NUMBER: 60/211,314  
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 ; PRIOR APPLICATION NUMBER: 60/219,007  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: 60/255,281  
 ; PRIOR FILING DATE: 2000-12-13  
 ; NUMBER OF SEQ ID NOS: 62232  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 40351  
 ; LENGTH: 407  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-357-930-40351

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 Qy 1955 GTACCTTCTCAGAGTCTTCGGTTGGTCTCAACAATCTCTAGACCTCTCTGGAAGATG 2014

Db 374 GTACCTTCTCAGAGTCTTCGGTTGGTCTCAACAATCTCTAGACCTCTCTGGAAGATG 315  
 Qy 2015 GTGCTCTGGAGAGCCAGATACAGAGATCTCCAGTTTACACTATCAGAGGAGAACCGTT 2074  
 Db 314 GTGCTCTGGAGAGCCAGATACAGAGATCTCCAGTTTACACTATCAGAGGAGAACCGTT 255  
 Qy 2075 CTGAAGGAAAAGTTGGTTTTCAGGCCCTATAGAAATTAATCTTTCAGAGCTGGTGTCTCAGTGA 2134  
 Db 254 CTGAAGGAAAAGTTGGTTTTCAGGCCCTATAGAAATTAATCTTTCAGAGCTGGTGTCTCAGTGA 195  
 Qy 2135 TTGCTTTCAATTTTCTTAATCTTCTTAACACTGCAGCTCAGGTTGCTATGTGCTTCAAG 2194  
 Db 194 TTGCTTTCAATTTTCTTAATCTTCTTAACACTGCAGCTCAGGTTGCTATGTGCTTCAAG 135  
 Qy 2195 ATTGCTGGCTTTCATCTACTGGGCAACCAACAAAGATATGCTAAATGTCACCTGTAATGAG 2254  
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 ; Publication No. US20040259086A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schlegel, Robert  
 ; APPLICANT: Endege, Wilson  
 ; APPLICANT: Monahan, John  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER  
 ; FILE REFERENCE: MRI-007BCN  
 ; CURRENT APPLICATION NUMBER: US/10/357,930  
 ; CURRENT FILING DATE: 2003-02-04  
 ; PRIOR APPLICATION NUMBER: 09/785,276  
 ; PRIOR FILING DATE: 2003-02-16  
 ; PRIOR APPLICATION NUMBER: 60/183,319  
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 ; PRIOR FILING DATE: 2000-05-25  
 ; PRIOR APPLICATION NUMBER: 60/211,314  
 ; PRIOR FILING DATE: 2000-06-09  
 ; PRIOR APPLICATION NUMBER: 60/219,007  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: 60/255,281  
 ; PRIOR FILING DATE: 2000-12-13  
 ; NUMBER OF SEQ ID NOS: 62232  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 24228  
 ; LENGTH: 442  
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 ; ORGANISM: Homo sapiens  
 US-10-357-930-24228

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Qy 772 TTCTCATCTAGGAGTAAACTGCAACTTTCACGGATGCCAGATCAGGACCATGAAT 831  
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RESULT 4  
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; Sequence 41929, Application US/10357930  
; Publication No. US20040259086A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Endege, Wilson  
; APPLICANT: Monahan, John  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
; TITLE OF INVENTION: HUMAN PROSTATE CANCER  
; FILE REFERENCE: MRI-007BCN  
; CURRENT APPLICATION NUMBER: US/10/357,930  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: 09/785,276  
; PRIOR FILING DATE: 2003-02-16  
; PRIOR APPLICATION NUMBER: 60/183,319  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 60/189,862  
; PRIOR FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/207,454  
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; PRIOR APPLICATION NUMBER: 60/211,314  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/219,007  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: 60/255,281  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 62232  
; SOFTWARE: PastSeq for Windows Version 4.0  
; SEQ ID NO 41929  
; LENGTH: 425  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-357-930-41929

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Best Local Similarity 100.0%; Pred. No. 6.3e-124;  
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 234 CTGTCCAATGATGTGAACAAGTTTGAATCAGGTGACAGTGTCTTTACACTTCTCTGGGCA 293

Qy 652 GGACCACTGACGGGATCGGATGACCTGCTCTGATGGATAGGATATCTGTC 711  
Db 294 GGACCACTGACGGGATCGGATGACCTGCTCTGATGGATAGGATATCTGTC 353

Qy 712 CTTCCTGGGATGGCAGTTCTTAATCATTTCTCTGCGCTTGCAAAGCTGTTTGGGAAGTTG 771  
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Qy 772 TTCTCATCACTG 783  
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Db 414 TTCTCATCACTG 425  
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; Sequence 823, Application US/09759143  
; Patent No. US20020022248A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: PastSeq for Windows Version 3.0  
; SEQ ID NO 823  
; LENGTH: 291  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-759-143-823

Query Match 5.4%; Score 216; DB 9; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.4e-104;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAAATTTGCCCACTGCCCTGCTAACCACTGACACAGATTGAACACCAATT 3714  
Db 7 ATCCGGAGAAATTTGCCCACTGCCCTGCTAACCACTGACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCAGACAGATTAATGGTTTATAGATTCAGGAAGACTGAAGAATATATGATGAGCG 3774  
Db 67 ATTGACAGCAGACAGATTAATGGTTTATAGATTCAGGAAGACTGAAGAATATATGATGAGCG 126

Qy 3775 TATGTTTTGCTGCAAAATAAAGAGAGCTATTTTACAAAGATGGTGCAACTGGGCAAG 3834  
Db 127 TATGTTTTGCTGCAAAATAAAGAGAGCTATTTTACAAAGATGGTGCAACTGGGCAAG 186

Qy 3835 GCAGAGCCGCTGCGCTTCACTCTGAAACAGCAAAACAG 3870  
Db 187 GCAGAGCCGCTGCGCTTCACTCTGAAACAGCAAAACAG 222

RESULT 6  
US-09-780-669-823  
; Sequence 823, Application US/09780669  
; Patent No. US2002005197A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.

```

; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-823

Query Match      5.4%; Score 216; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCACTGACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGGAGAAATTTGCCACTGACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 3774
Db 67 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 126

Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 3834
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 186

Qy 3835 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 222

US-09-822-827-823
US-09-822-827-823
; Sequence 823, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-823

Query Match      5.4%; Score 216; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCACTGACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGGAGAAATTTGCCACTGACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 3774
Db 67 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 126

Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 3834
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 186

Qy 3835 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 222

US-09-895-793-823
US-09-895-793-823
; Sequence 823, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-823

Query Match      5.4%; Score 216; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCACTGACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGGAGAAATTTGCCACTGACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 3774
Db 67 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 126

Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 3834
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 186

Qy 3835 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 222

```

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Db 67 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 126
Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 3834
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 186
Qy 3835 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 222

RESULT 8
US-09-895-793-823
; Sequence 823, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-823

Query Match      5.4%; Score 216; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGGAGAAATTTGCCACTGACCGTGTAAACCAATTCACACAGATTGAACACCAATT 3714
Db 7 ATCCGGGAGAAATTTGCCACTGACCGTGTAAACCAATTCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 3774
Db 67 ATTGACAGCGACGAAGATAATGGTTTAGATTTCAGAAAGACTGAAAGAAATATGATGAGCGG 126

Qy 3775 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 3834
Db 127 TATGTTTGTGCAAAATAAAGAGAGCGCTATTTTACAGATGGTGCAACCACTGGGCAAG 186

Qy 3835 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 3870
Db 187 GCAGAGCCCGTGCCTCCTCCTGAAACAGCAAAACAG 222

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RESULT 9

US-09-895-814-823  
; Sequence 823, Application US/09895814  
; Publication No. US20020193296A1  
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqiu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Fanger, Gary R.  
APPLICANT: Foy, Teresa  
APPLICANT: Wantanabe, Yoshihiro  
APPLICANT: Meagher, Madeleine Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C26  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 990  
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 823  
; LENGTH: 291  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-895-814-823

Query Match 5.4%; Score 216; DB 9; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.4e-104;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714  
Db 7 ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 3774  
Db 67 ATTGACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 126

Qy 3775 TATGTTTTGTCGCAAAATAAAGAGAGCCTATTTTACAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTTGTCGCAAAATAAAGAGAGCCTATTTTACAGATGGTGCAACAACTGGGCAAG 186

Qy 3835 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 222

RESULT 10

US-10-012-896-823  
; Sequence 823, Application US/10012896  
; Publication No. US20020183251A1  
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqiu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Fanger, Gary R.  
APPLICANT: Foy, Teresa  
APPLICANT: Wantanabe, Yoshihiro  
APPLICANT: Meagher, Madeleine Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C27  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 1011  
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 823  
; LENGTH: 291  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-012-896-823

Query Match 5.4%; Score 216; DB 13; Length 291;  
Best Local Similarity 100.0%; Pred. No. 1.4e-104;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3655 ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 3714  
Db 7 ATCCGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTGCACACAGATTGAACACCAATT 66

Qy 3715 ATTGACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 3774  
Db 67 ATTGACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGGAAGAAATATGATGAGCCG 126

Qy 3775 TATGTTTTGTCGCAAAATAAAGAGAGCCTATTTTACAGATGGTGCAACAACTGGGCAAG 3834  
Db 127 TATGTTTTGTCGCAAAATAAAGAGAGCCTATTTTACAGATGGTGCAACAACTGGGCAAG 186

Qy 3835 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 3870  
Db 187 GCAGAAGCCGCTGCCCTCACTGAAACAGCAAAACAG 222

RESULT 11

US-10-144-678A-823  
; Sequence 823, Application US/10144678A  
; Publication No. US20030157089A1  
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqiu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A. W.  
APPLICANT: Hepler, William T.



```
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-144-678A-823

Query Match      5.4%; Score 216; DB 16; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3655 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCGACACAGATTGAACACCAATT 3714
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      3715 ATTCACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 3774
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      3775 TATGTTTCTGCGAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACACTGGGCAAG 3834
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      3835 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 3870
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
187 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 222

RESULT 12
US-10-294-025-823
; Sequence 823, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 823
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-294-025-823

Query Match      5.4%; Score 216; DB 16; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3655 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCGACACAGATTGAACACCAATT 3714
Db      7 ATCCGGGAGAAATTTGCCCACTGCACCGTGTAAACCAATTCGACACAGATTGAACACCAATT 66
;
Qy      3715 ATTCACAGCGCAAGATAATGGTTTTAGATTTCAGGAAGACTGAAAGAAATATGATGAGCGG 3774
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      3775 TATGTTTCTGCGAAAATAAAGAGAGCGCTATTTTACAAGATGGTGCAACACTGGGCAAG 3834
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      3835 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 3870
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
187 GCAGAGCGCGTGCCTCCTCACTGAAACAGCAAAACAG 222

RESULT 13
US-10-357-930-41689
; Sequence 41689, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41689
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-357-930-41689

Query Match      5.3%; Score 210; DB 18; Length 391;
Best Local Similarity 100.0%; Pred. No. 2.5e-101;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      532 GCACCTTCGTCCTTAGTAACATGGCCATGGGGAAGACAACCAAGAGATAGTCAATCTG 591
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      167 GCACCTTCGTCCTTAGTAACATGGCCATGGGGAAGACAACCAAGAGATAGTCAATCTG 226
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      592 CTGTCCAATGATGTGAACAAGTTTGATCAGTGACAGTGTCTTACACTTCTCTGTGGGCA 651
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      227 CTGTCCAATGATGTGAACAAGTTTGATCAGTGACAGTGTCTTACACTTCTCTGTGGGCA 286
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      652 GGACCACTGCAGGCGATCGCAGTGACCTGCTCTCTGGATGGAGATAGGAATATCGTGC 711
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      287 GGACCACTGCAGGCGATCGCAGTGACCTGCTCTCTGGATGGAGATAGGAATATCGTGC 346
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
Qy      712 CTGTCTGGGATGGCAGTTCTTAATCAATTCTC 741
Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
;
347 CTGTCTGGGATGGCAGTTCTTAATCAATTCTC 376

RESULT 14
US-10-357-930-32647
; Sequence 32647, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
```

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; APPLICANT: Endege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32647
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-32647

Query Match      5.2%; Score 208; DB 18; Length 444;
Best Local Similarity 100.0%; Pred. No. 3e-100;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 568 ACCACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGTGAACAAGTTTGATCAGGTGACA 627
Db 225 ACCACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGTGAACAAGTTTGATCAGGTGACA 284

Qy 628 GTGTTCTTACACTTCTCTGGGAGGACCACTGCGAGGCGATCGCAGTGCCTACTC 687
Db 285 GTGTTCTTACACTTCTCTGGGAGGACCACTGCGAGGCGATCGCAGTGCCTACTC 344

Qy 688 TGGATGGAGATAGGAATATCGTCTGCTGGGATGGCAGTTCTAATCATTTCTCTGCCCC 747
Db 345 TGGATGGAGATAGGAATATCGTCTGCTGGGATGGCAGTTCTAATCATTTCTCTGCCCC 404

Qy 748 TTGCAAGCTGTTTGGGAAGTTGTTCT 775
Db 405 TTGCAAGCTGTTTGGGAAGTTGTTCT 432

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# RESULT 15

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US-10-357-930-11475
; Sequence 11475, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25

```

```

; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11475
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-11475

Query Match      5.2%; Score 208; DB 18; Length 482;
Best Local Similarity 100.0%; Pred. No. 3e-100;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 568 ACCACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGTGAACAAGTTTGATCAGGTGACA 627
Db 180 ACCACAGCCAGATAGTCAATCTGCTGTCCTCAATGATGTGAACAAGTTTGATCAGGTGACA 239

Qy 628 GTGTTCTTACACTTCTCTGGGAGGACCACTGCGAGGCGATCGCAGTGCCTACTC 687
Db 240 GTGTTCTTACACTTCTCTGGGAGGACCACTGCGAGGCGATCGCAGTGCCTACTC 299

Qy 688 TGGATGGAGATAGGAATATCGTCTGCTGGGATGGCAGTTCTAATCATTTCTCTGCCCC 747
Db 300 TGGATGGAGATAGGAATATCGTCTGCTGGGATGGCAGTTCTAATCATTTCTCTGCCCC 359

Qy 748 TTGCAAGCTGTTTGGGAAGTTGTTCT 775
Db 360 TTGCAAGCTGTTTGGGAAGTTGTTCT 387

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Search completed: May 20, 2005, 03:46:49  
Job time : 2180 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2005, 18:21:20 ; Search time 12058 Seconds  
(without alignments)  
12557.610 Million cell updates/sec

Title: US-09-976-858-41

Perfect score: 3978

Sequence: 1 atgtgcgcgtgtaccagga.....ttttcgagacagcactgtga 3978

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 29252628

Minimum DB seq length: 0

Maximum DB seq length: 500

Post-processing: Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gss1.\*
- 9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	491	12.3	491	5 BX474791	BX474791 DKFZp686G
2	472	11.9	497	1 AL701816	AL701816 DKFZp686F
3	435	10.9	435	2 BE327296	BE327296 hw10b05.x
4	406	10.2	465	1 AU126646	AU126646 AU126646
5	361	9.1	478	2 BE674208	BE674208 7d76g07.x
6	341	8.6	447	7 CN410193	CN410193 170005321
7	294	7.4	383	7 R35797	R35797 YG66a11.r1
8	234	5.9	367	1 AA305627	AA305627 EST176623
9	198	5.0	387	2 BE769452	BE769452 QV3-FT003
10	178	4.5	348	2 BE838702	BE838702 RC6-FN011
11	178	4.5	405	2 BE838708	BE838708 RC6-FN011
12	178	4.5	413	2 BE838700	BE838700 RC6-FN011
13	178	4.5	443	2 BE838704	BE838704 RC6-FN011
14	177	4.4	415	2 BE838700	BE838700 RC6-FN011
15	175	4.4	377	2 BE838720	BE838720 RC6-FN011
16	149	3.7	254	2 BE769429	BE769429 FM4-FT002
17	145	3.6	405	2 BE838733	BE838733 RC6-FN011
18	145	3.6	482	7 R00050	R00050 YG70605.s1
19	137	3.4	290	1 AA375392	AA375392 EST87662
20	132	3.3	344	2 BE838696	BE838696 RC6-FN011
21	131	3.3	411	2 BE838692	BE838692 RC6-FN011
22	128	3.2	179	2 BE765041	BE765041 IL2-NT009
23	117	2.9	252	8 CC325199	CC325199 XL153 Bay
24	113	2.8	329	2 BE838725	BE838725 RC6-FN011

c	25	110	2.8	326	2	BE769242	BE769242 PM4-FT002
	26	99	2.5	310	2	BF360747	BF360747 QV2-OT006
	27	97	2.4	357	8	AQ088953	AQ088953 HS_3004 B
	28	74	1.9	124	2	BE153864	BE153864 PM0-HT033
	29	72	1.8	190	2	BE174699	BE174699 QV2-HT057
	30	59	1.5	133	1	AI569098	AI569098 tr82a09.x
	31	53	1.3	351	2	BE838707	BE838707 RC6-FN011
	32	50	1.3	336	8	AQ088957	AQ088957 HS_3004 B
	33	41	1.0	418	1	AJ683278	AJ683278 RC3-HT023
	34	39	1.0	415	2	BF836367	BF836367 RC3-HT023
	35	38	1.0	132	9	CG869157	CG869157 AC0303 Sa
	36	38	1.0	175	9	CC894135	CC894135 RRR160 Ba
	37	38	1.0	362	7	CK337853	CK337853 C0347H04
	38	38	1.0	406	4	BI403742	BI403742 MI-P-CF1-
	39	36	0.9	487	2	BF231451	BF231451 253864 BA
	40	35	0.9	264	2	BE838685	BE838685 RC6-FN011
	41	35	0.9	465	4	BI540773	BI540773 454162 MA
	42	33	0.8	157	2	BE769293	BE769293 PM4-FT002
	43	33	0.8	380	4	BI044374	BI044374 PM4-OT021
	44	33	0.8	469	7	CN677720	CN677720 E0101B09-
	45	32	0.8	453	4	BM287170	BM287170 527468 MA

#### ALIGNMENTS

RESULT 1  
BX474791 491 bp mRNA linear EST 04-SEP-2003  
LOCUS DKFZp686G03172\_r1.686 (synonym: hlcc3) Homo sapiens cDNA clone  
DEFINITION DKFZp686G03172 5', mRNA sequence.  
ACCESSION BX474791  
VERSION BX474791.1 GI:31668993  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Bloembergen, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobos, G., Han, M. and Wiemann, S.  
TITLE EST (Bloembergen, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert.  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686G03172) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

#### FEATURES

Location/Qualifiers  
1..491  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686G03172"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlcc3)"  
/note="vector: pTriplex2; Site\_1: SfIIA; Site\_2: SfiIB; cDNA-collection"

#### ORIGIN

Query Match 12.3%; Score 491; DB 5; Length 491;  
Best Local Similarity 100.0%; Pred. No. 7e-257;  
Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1906 GAGGAAAGTGAACACCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCA 1965
Db 1 GAGGAAAGTGAACACCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCA 60

Qy 1966 GAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCCCTCTTGAAGATGGTCTCTGGAG 2025
Db 61 GAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCCCTCTTGAAGATGGTCTCTGGAG 120

Qy 2026 AGCCAAAGTACAGGAATGTCCTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAA 2085
Db 121 AGCCAAAGTACAGGAATGTCCTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAA 180

Qy 2086 GTTGGTTTTCAGGCTTAAGAAATTAATCTCAGAGCTGGTGTCTCACTGGATTGTCTTCATT 2145
Db 181 GTTGGTTTTCAGGCTTAAGAAATTAATCTCAGAGCTGGTGTCTCACTGGATTGTCTTCATT 240

Qy 2146 TTCCTTAATCTCTAAACACTGCAGCTCAGCTTGCCTATGTGCTTCAAGATTGGTGGCTT 2205
Db 241 TTCCTTAATCTCTAAACACTGCAGCTCAGCTTGCCTATGTGCTTCAAGATTGGTGGCTT 300

Qy 2206 TCATATGGGCAACAAACAAGTATGCTAAATGCTACTGTAATGAGGAGGAAATGTA 2265
Db 301 TCATATGGGCAACAAACAAGTATGCTAAATGCTACTGTAATGAGGAGGAAATGTA 360

Qy 2266 ACCGAGAGCTAGATCTTAACTGGTACTTAGCAATTTATTTCAGGTTTAACTGTAGCTACC 2325
Db 361 ACCGAGAGCTAGATCTTAACTGGTACTTAGCAATTTATTTCAGGTTTAACTGTAGCTACC 420

Qy 2326 GTTCTTTTGGCATAGCAAGATCTATTGGTATTCTACGCTCTTGTGTTAACTCTTCAAA 2385
Db 421 GTTCTTTTGGCATAGCAAGATCTATTGGTATTCTACGCTCTTGTGTTAACTCTTCAAA 480

Qy 2386 ACTTTGCACAA 2396
Db 481 ACTTTGCACAA 491

RESULT 2
AL701816 497 bp mRNA linear EST 04-SEP-2003
LOCUS DKFP686F08149.r1.686 (synonym: hlcc3) Homo sapiens cdna clone
DEFINITION DKFP686F08149 5', mRNA sequence.
ACCESSION AL701816
VERSION AL701816.1 GI:19685172
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)
Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cdna sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFP686F08149) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1. 497
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP686F08149"
/dev_stages="adult"
/lab_host="DH10B"
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ORIGIN
Query Match 11.9%; Score 472; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.9e-246;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1466 TGAGGAGTAATATTTATTTTGGGAGAAATACGAAAAGAACGATATGAAAAAGTCATAA 1525
Db 1 TGAGGAGTAATATTTATTTTGGGAGAAATACGAAAAGAACGATATGAAAAAGTCATAA 60

Qy 1526 AGCTCTGCTCTCAAAAAGGATTTACAGCTGTGTGGAGGATGGTGACTGCTGTGATAG 1585
Db 61 AGCTCTGCTCTCAAAAAGGATTTACAGCTGTGTGGAGGATGGTGACTGCTGTGATAG 120

Qy 1586 GAGATCCGGGAACCCACGCTGAGTGGAGGCGAGAAAGCACCGGTAAACCTTGCAGAGAGCAG 1645
Db 121 GAGATCCGGGAACCCACGCTGAGTGGAGGCGAGAAAGCACCGGTAAACCTTGCAGAGAGCAG 180

Qy 1646 TGTATCAAGATGCTGACATCTCTCTCGACGATCCCTCAGTGCAGTAGATCGGGAAG 1705
Db 181 TGTATCAAGATGCTGACATCTCTCTCGACGATCCCTCAGTGCAGTAGATCGGGAAG 240

Qy 1706 TTAGCAGACACTTGTTCGAACTGTGTATTGTCAAAATTTTGCATGAGAAGATCAAAATTT 1765
Db 241 TTAGCAGACACTTGTTCGAACTGTGTATTGTCAAAATTTTGCATGAGAAGATCAAAATTT 300

Qy 1766 TAGTGACTCATCAGTTGTCAGTACCTCAAAGCTGCAAGTCAGATTTCTGATATTGAAAGATG 1825
Db 301 TAGTGACTCATCAGTTGTCAGTACCTCAAAGCTGCAAGTCAGATTTCTGATATTGAAAGATG 360

Qy 1826 GTAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAATCTGGTATAGATTTTGGCT 1885
Db 361 GTAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAATCTGGTATAGATTTTGGCT 420

Qy 1886 CCCTTTTAAAGNAGGATAATCAGGAAAGTGAACAACCTCCAGTTCAGGAGAC 1937
Db 421 CCCTTTTAAAGNAGGATAATCAGGAAAGTGAACAACCTCCAGTTCAGGAGAC 472

RESULT 3
BE327296/c 435 bp mRNA linear EST 14-JUL-2000
LOCUS hwi0505.x1 NCI CGAP Lu24 Homo sapiens cdna clone IMAGE:3182481 3'
DEFINITION similar to TR:075555 ABC TRANSPORTER MOAT-B ISOFORM ;, mRNA
sequence.
ACCESSION BE327296
VERSION BE327296.1 GI:9201072
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cdna Library Preparation: M. Bento Soares, Ph.D.
cdna Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E.; Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 424.
Location/Qualifiers
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source      1. 435
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3182481"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu24"
/notes="Organ: lung; Vector: p7T73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP Lu5 was prepared, and as circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clones
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Query Match      10.9%; Score 435; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 3.8e-226;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3211 GTTGGCAATGTGGAGAACCGGAGCTGGAAAAGTTCCCTCATCTCAGCCCTTTTAGA 3270
|
Db 435 GTTGGCAATGTGGAGAACCGGAGCTGGAAAAGTTCCCTCATCTCAGCCCTTTTAGA 376
|
Qy 3271 TTGTGACAGACCCGAGGTAAATTTGGATTGATGAAGATCTTGACAACTGAAATTTGGACTT 3330
|
Db 375 TTGTGACAGACCCGAGGTAAATTTGGATTGATGAAGATCTTGACAACTGAAATTTGGACTT 316
|
Qy 3331 CACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTTTTGTTCACTGGGAACA 3390
|
Db 315 CACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTTTTGTTCACTGGGAACA 256
|
Qy 3391 ATGAGGAAAACCTGGATCCCTTTAATGAGCACACGATGAGGAACCTGTGGAATGCCCTTA 3450
|
Db 255 ATGAGGAAAACCTGGATCCCTTTAATGAGCACACGATGAGGAACCTGTGGAATGCCCTTA 196
|
Qy 3451 CAAGAGGTACAACTTAAAGAAACCATTTGAAGATCTCTCGTAAATGGATCTGAATTA 3510
|
Db 195 CAAGAGGTACAACTTAAAGAAACCATTTGAAGATCTCTCGTAAATGGATCTGAATTA 136
|
Qy 3511 GCAGAAATCAGGATCCAAATTTTAGTGTGGACAAAGACAACTGTGTGCTTGCACAGGCGCA 3570
|
Db 135 GCAGAAATCAGGATCCAAATTTTAGTGTGGACAAAGACAACTGTGTGCTTGCACAGGCGCA 76
|
Qy 3571 ATTCTAGGAAAATCAGATATTGATTTAGTGAAGCGGCGCAAAATGTGGATCCAAAGA 3630
|
Db 75 ATTCTAGGAAAATCAGATATTGATTTAGTGAAGCGGCGCAAAATGTGGATCCAAAGA 16
|
Qy 3631 ACTGATCAGTTAATA 3645
|
Db 15 ACTGATCAGTTAATA 1
|

RESULT 4
LOCUS      AUI26646
DEFINITION AUI26646 NT2RP1 Homo sapiens cdna clone NT2RP1001350 5', mRNA
sequence.
ACCESSION AUI26646
VERSION    AUI26646.1 GI:10951362
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 465)
Oca,T., Nishikawa,T., Suzuki,Y., Kawai,Y., Ishii,S., Saito,K.,
Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
HRI human cDNA project (Oca,T., Nishikawa,T., Suzuki,Y., Kawai,Y.,
Ishii,S., Saito,K., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)

```

```

Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
source      1. 465
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP1001350"
/cell_type="teratocarcinoma"
/notes="Vector: pUC19FL3; mRNA from NT2 neuronal precursor
cells after 48-hours retinoic acid (RA) induction"

ORIGIN
Query Match      10.2%; Score 406; DB 1; Length 465;
Best Local Similarity 100.0%; Pred. No. 3.2e-210;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3365 AGGAACTGTTTGTTCACCTGGAACATGAGAAAACCTGGATCCCTTTAATGAGCACA 3424
|
Db 14 AGGAACTGTTTGTTCACCTGGAACATGAGAAAACCTGGATCCCTTTAATGAGCACA 73
|
Qy 3425 CGGATGAGGAACCTGGAATGCCCTTACAAGAGGTACAACTTAAAGAACCACTTGAAGATC 3484
|
Db 74 CGGATGAGGAACCTGGAATGCCCTTACAAGAGGTACAACTTAAAGAACCACTTGAAGATC 133
|
Qy 3485 TTCCTGTTAAATGGATACCTGAATTTAGCAGAAATCAGGATCCAAATTTAGTGTGGACAAA 3544
|
Db 134 TTCCTGTTAAATGGATACCTGAATTTAGCAGAAATCAGGATCCAAATTTAGTGTGGACAAA 193
|
Qy 3545 GACAACTGTTGTGCTTGCAGGCAATTTCTCAGGAAAATCAGATATTGATTTATGATG 3604
|
Db 194 GACAACTGTTGTGCTTGCAGGCAATTTCTCAGGAAAATCAGATATTGATTTATGATG 253
|
Qy 3605 AAGCGAGCGCAAAATGTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGGGAGA 3664
|
Db 254 AAGCGAGCGCAAAATGTGGATCCAGAACTGATGAGTTAATACAAAAAATCCGGGAGA 313
|
Qy 3665 AATTGCCCCACTGCACCGCTGCTAACCAATTGCACACAGATTGCAACCACTTATTGACGCG 3724
|
Db 314 AATTGCCCCACTGCACCGCTGCTAACCAATTGCACACAGATTGCAACCACTTATTGACGCG 373
|
Qy 3725 ACAAGATAATGGTTTGTAGATTTCAGGAAGACTGAAAGAATATGATGA 3770
|
Db 374 ACAAGATAATGGTTTGTAGATTTCAGGAAGACTGAAAGAATATGATGA 419
|

RESULT 5
LOCUS      BE674208/c
DEFINITION BE674208.1 GI:10034749
sequence.
ACCESSION BE674208
VERSION    BE674208.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

```

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 446.  
FEATURES  
source  
1. .478  
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/organism="Homo sapiens"  
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/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lu24"  
/note="Organ: lung; Vector: pTT3D-Pac (Pharmacia) with a  
modified polylinker; Plasmid DNA from the normalized  
library NCI CGAP Lu5 was prepared, and as circles were  
made in vitro. Following HAP purification, this DNA was  
used as tracer in a subtractive hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (cloneIDs  
141920-1417991 and 1520904-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 9.1%; Score 361; DB 2; Length 478;  
Best Local Similarity 100.0%; Pred. No. 1.6e-185;  
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3283 GAAGTAAATTTGGATTGATAGATCTTGACAACTGAAATGGACTTCACGATTTAAGG 3342  
Db 367 GAAGTAAATTTGGATTGATAGATCTTGACAACTGAAATGGACTTCACGATTTAAGG 308  
Qy 3343 AAGAAATGTCATACCTCAGAACCTGTTTGTTCATCTGGAACATGAGGAAAAAC 3402  
Db 307 AAGAAATGTCATACCTCAGAACCTGTTTGTTCATCTGGAACATGAGGAAAAAC 248  
Qy 3403 CTGGATCCCTTTAATGACACACGATGAGCAACTGTGGAATGCTTACAGAGGTACAA 3462  
Db 247 CTGGATCCCTTTAATGACACACGATGAGCAACTGTGGAATGCTTACAGAGGTACAA 188  
Qy 3463 CTTAAAGAAACATTGAAGATCTTCCTGGTAAATGGATAGTAACTAGCAGATCAGGA 3522  
Db 187 CTTAAAGAAACATTGAAGATCTTCCTGGTAAATGGATAGTAACTAGCAGATCAGGA 128  
Qy 3523 TCCAAATTTAGTTGGCAAGAACAATGTTGTGCTTGCAGGCGCAATCTCAGGAAA 3582  
Db 127 TCCAAATTTAGTTGGCAAGAACAATGTTGTGCTTGCAGGCGCAATCTCAGGAAA 68  
Qy 3583 AATCAGATATTGATTATTGATGAAGCGACGCAATGGAATCCAAAGAACTGATGAGTTA 3642  
Db 67 AATCAGATATTGATTATTGATGAAGCGACGCAATGGAATCCAAAGAACTGATGAGTTA 8  
Qy 3643 A 3643  
Db 7 A 7

RESULT 6  
CN410193  
LOCUS CN410193 447 bp mRNA linear EST 16-MAY-2004  
DEFINITION 17000532183702 GRN\_ES Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN410193

VERSION CN410193.1 GI:47397317  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J and Stanton, L.W.  
TITLE Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert length: 447 Std Error: 0.00.

FEATURES

source  
1. .447  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/tissue\_type="embryonic stem cells, cell lines H1, H7, and  
H9"  
/clone\_lib="GRN ES"  
/note="oligo dt primed, full-length enriched cDNA library  
from undifferentiated hES cell lines H1 (p32), H7 (p29),  
and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 8.6%; Score 341; DB 7; Length 447;  
Best Local Similarity 99.7%; Pred. No. 1.5e-174;  
Matches 391; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 559 GGGGAAGACACCAAGCCAGATAGTCAATCTGCTGCCAATGATGTGAACAAGTTTGAT 618  
Db 1 GGGGAAGACACCAAGCCAGATAGTCAATCTGCTGCCAATGATGTGAACAAGTTTGAT 60  
Qy 619 CAGGTGACAGTGTCTTACACTTCTCTGGCGAGACCACTGCAGGCGATCGCAGTGACT 678  
Db 61 CAGGTGACAGTGTCTTACACTTCTCTGGCGAGACCACTGCAGGCGATCGCAGTGACT 120  
Qy 679 GCCCTACTCTGGATGGAGATAGGAATATCGTCCCTTCTGGATGGCAGTTCTAATCAT 738  
Db 121 GCCCTACTCTGGATGGAGATAGGAATATCGTCCCTTCTGGATGGCAGTTCTAATCAT 180  
Qy 739 CTCCTGCCCTTGCAAAAGCTGTTTGGGAAGTGTGTTCTCATCCTGAGGAGTAAACTGCA 798  
Db 181 CTCCTGCCCTTGCAAAAGCTGTTTGGGAAGTGTGTTCTCATCCTGAGGAGTAAACTGCA 240  
Qy 799 ACTTTCACGGATGCCAGGATCAGACCATGAATGAAGTTAATCTGTTAAGGATATA 858  
Db 241 ACTTTCACGGATGCCAGGATCAGACCATGAATGAAGTTAATCTGTTAAGGATATA 300  
Qy 859 AAAATGTACGCTGGGAAAAGTCAATTTCAAATCTTATTACCAATTTGAGAAAGAGAG 918  
Db 301 AAAATGTACGCTGGGAAAAGTCAATTTCAAATCTTATTACCAATTTGAGAAAGAGAG 360  
Qy 919 ATTTCCAAAGATTTGAGAAAGTTCTCGCTCAG 950  
Db 361 ATTTCCAAAGATTTGAGAAAGTTCTCGCTCAG 392

RESULT 7

R35797  
LOCUS R35797 383 bp mRNA linear EST 02-MAY-1995  
DEFINITION YG66a11.t1 Soares infant brain INIB Homo sapiens cDNA clone  
IMAGE:38089 5', similar to SP:MRP HUMAN P33527 MULTIDRUG  
RESISTANCE-ASSOCIATED ;, mRNA sequence.





Db 61 AGATGTCCTCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTTCAGG 120

Qy 2099 CCTATAAGAAATTACTTCCAGAGCTGGTGTCTACTGGATGTCTTCATTTCTTATTTCTCC 2158

Db 121 CCTATAAGAAATTACTTCCAGAGCTGGTGTCTACTGGATGTCTTCATTTCTTATTTCTCC 180

Qy 2159 TAAACACTGCAGCTCAGGTTGGCTTATGCTTCAAGATTCGTTGCTTTCATACCTGGGCAA 2218

Db 181 TAAACACTGCAGCTCAGGTTGGCTTATGCTTCAAGATTCGTTGCTTTCATACCTGGGCAA 240

Qy 2219 ACAACAAAGTATCTAAATGCTACTGTAATGAGGAGGAGAAATGTAACCGAGAGCTAG 2278

Db 241 ACAACAAAGTATCTAAATGCTACTGTAATGAGGAGGAGAAATGTAACCGAGAGCTAG 300

Qy 2279 ATCTTAACCTGCTACTTATAGGAATTTATTACAGGTTTAACTGTAGCTTACCGTTCTTTTGGCA 2338

Db 301 ATCTTAACCTGCTACTTATAGGAATTTATTACAGGTTTAACTGTAGCTTACCGTTCTTTTGGCA 360

Qy 2339 TAGCAAGATCTCTATTGTTCTTACG 2365

Db 361 TAGCAAGATCTCTATTGTTCTTACG 387

RESULT 9  
LOCUS BE769452 367 bp mRNA linear EST 20-SEP-2000  
DEFINITION QV3-FT0032-190700-269-e09 FT0032 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE769452  
VERSION BE769452.1 GI:10223110  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 367)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2-QV3-FT0032-190700-269-e09&tl=2000-07-19&tl=1)  
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High quality sequence stop: 367.  
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FEATURES  
source  
1. .367  
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ORIGIN  
Query Match 5.0%; Score 198; DB 2; Length 367;  
Best Local Similarity 100.0%; Pred. No. 4.7e-96;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2687 CTGGAGTCCAGTGTGTTTCCACTTGTCTCTCTCCAGGGGCTCTGGACCATCCGG 2746  
Db 170 CTGGAGTCCAGTGTGTTTCCACTTGTCTCTCTCCAGGGGCTCTGGACCATCCGG 229  
Qy 2747 CATACAAGCAGAGAGAGGTGTGAGAACTGTTTGTATGCACACACAGGATTTACATTCAG 2806  
Db 230 CATACAAGCAGAGAGAGGTGTGAGAACTGTTTGTATGCACACAGGATTTACATTCAG 289  
Qy 2807 AGGCTTGGTCTTCTTTTGGACAACTGTCCTGCTGCTGCTGATGCCATCT 2866  
Db 290 AGGCTTGGTCTTCTTTTGGACAACTGTCCTGCTGCTGCTGATGCCATCT 349  
Qy 2867 GTGCCATGTTTGTCAATCA 2884  
Db 350 GTGCCATGTTTGTCAATCA 367

RESULT 10  
LOCUS BE838702 348 bp mRNA linear EST 22-SEP-2000  
DEFINITION RC6-FN0112-190700-011-B08 FN0112 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE838702  
VERSION BE838702.1 GI:10271080  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 348)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2-RC6-FN0112-190700-011-B08&tl=2000-07-19&tl=1)  
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High quality sequence start: 4  
High quality sequence stop: 347.  
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/note="Organ: prostate normal; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent

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/organism="Homo sapiens"  
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/clone\_lib="FN0112"  
/note="Organ: prostate normal; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 4.5%; Score 178; DB 2; Length 348;  
 Best Local Similarity 100.0%; Pred. NO. 4.5e-85;  
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2918 CTCGTGATCGCGGACAGTTGGTTTGGCACTGTCTATGCCCTCACGCTCATGGGATGT 2977  
 Db 222 CTCGTGATCGCGGACAGTTGGTTTGGCACTGTCTATGCCCTCACGCTCATGGGATGT 163  
 Qy 2978 TTCAGTGGTGTTCGACAAAGTCTCGAAGTTGAGAATATGATGATCTCAGTAGAAGGG 3037  
 Db 162 TTCAGTGGTGTTCGACAAAGTCTCGAAGTTGAGAATATGATGATCTCAGTAGAAGGG 103  
 Qy 3038 TCATTGAATACACAGACCTTGAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 3095  
 Db 102 TCATTGAATACACAGACCTTGAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 45

RESULT 11

BE838708/c

LOCUS BE838708 405 bp mRNA linear EST 22-SEP-2000

DEFINITION RC6-FN0112-190700-011-E02 FN0112 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE838708

VERSION BE838708.1 GI:10271086

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 405)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC6-FN0112-190  
 700-011-E02&t3=2000-07-19&t4=1)

Seq primer: puc 18 forward  
 High quality sequence start: 27  
 High quality sequence stop: 404.

FEATURES

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 /note="Organ: prostate normal; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 4.5%; Score 178; DB 2; Length 405;  
 Best Local Similarity 100.0%; Pred. NO. 4.5e-85;  
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2918 CTCGTGATCGCGGACAGTTGGTTTGGCACTGTCTATGCCCTCACGCTCATGGGATGT 2977  
 Db 227 CTCGTGATCGCGGACAGTTGGTTTGGCACTGTCTATGCCCTCACGCTCATGGGATGT 168  
 Qy 2978 TTCAGTGGTGTTCGACAAAGTCTCGAAGTTGAGAATATGATGATCTCAGTAGAAGGG 3037  
 Db 167 TTCAGTGGTGTTCGACAAAGTCTCGAAGTTGAGAATATGATGATCTCAGTAGAAGGG 108  
 Qy 3038 TCATTGAATACACAGACCTTGAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 3095  
 Db 107 TCATTGAATACACAGACCTTGAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 50

RESULT 12

BE838700/c

LOCUS BE838700 413 bp mRNA linear EST 22-SEP-2000

DEFINITION RC6-FN0112-190700-011-B03 FN0112 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE838700

VERSION BE838700.1 GI:10271078

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 413)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC6-FN0112-190  
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Seq primer: puc 18 forward  
 High quality sequence start: 12  
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FEATURES

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 /note="Organ: prostate normal; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 4.5%; Score 178; DB 2; Length 413;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-85;  
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2918 CTCGGATGCCGCGCAGTTGGTTGGCAGTCTGCTATGCTGCTATGCCCTCACGCTCATGGGGATGT 2977  
 Db 217 CTCGGATGCCGCGCAGTTGGTTGGCAGTCTGCTATGCTGCTATGCCCTCACGCTCATGGGGATGT 158

Qy 2978 TTCAGTGGTGTGTTTCGACAAAGTCTGCTGAGTGTGAGATATGATGATCTCAGTAGAAAAGG 3037  
 Db 157 TTCAGTGGTGTGTTTCGACAAAGTCTGCTGAGTGTGAGATATGATGATCTCAGTAGAAAAGG 98

Qy 3038 TCATTGAATACACAGACCTTGAAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 3095  
 Db 97 TCATTGAATACACAGACCTTGAAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 40

RESULT 13  
 BE838704/c  
 LOCUS BE838704 443 bp mRNA linear EST 22-SEP-2000  
 DEFINITION RC6-FN0112-190700-011-C04 FN0112 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BE838704  
 VERSION BE838704.1 GI:10271082  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 443)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC6-FN0112-190700-011-C04&t3=2000-07-19&t4=1)  
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 High quality sequence stop: 383.

## FEATURES

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 /note="Organ: prostate normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 4.4%; Score 177; DB 2; Length 415;  
 Best Local Similarity 99.6%; Pred. No. 1.6e-84;

## Query Match

Best Local Similarity 100.0%; Score 178; DB 2; Length 443;  
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2918 CTCGGATGCCGCGCAGTTGGTTGGCAGTCTGCTATGCTGCTATGCCCTCACGCTCATGGGGATGT 2977  
 Db 220 CTCGGATGCCGCGCAGTTGGTTGGCAGTCTGCTATGCTGCTATGCCCTCACGCTCATGGGGATGT 161

Qy 2978 TTCAGTGGTGTGTTTCGACAAAGTCTGCTGAGTGTGAGATATGATGATCTCAGTAGAAAAGG 3037  
 Db 160 TTCAGTGGTGTGTTTCGACAAAGTCTGCTGAGTGTGAGATATGATGATCTCAGTAGAAAAGG 101

Qy 3038 TCATTGAATACACAGACCTTGAAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 3095  
 Db 100 TCATTGAATACACAGACCTTGAAAAAGAACGACCTTGGGAATATCAGAAAGCCACC 43

RESULT 14  
BF836367/c

LOCUS BF836367 415 bp mRNA linear EST 13-JAN-2001  
 DEFINITION RC3-HT0230-171100-117-e08 HT0230 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF836367  
 VERSION BF836367.1 GI:12188188  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 415)  
 AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC3-HT0230-171100-117-e08&t3=2000-11-17&t4=1)  
 Seg primer: puc 18 forward  
 High quality sequence start: 41  
 High quality sequence stop: 415.

## FEATURES

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 /note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Matches 227; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 378 ACATTTAAGGAAGAAATGCAATCATACCTCAGGAACCTGTTTGTTCATCTGAACAA 319

Qy 3392 TGAGGAAAACCTGGATCCCTTTAATGAGCACACGGATGAGGAACCTGTGGAATCCCTTAC 3451

Db 318 TGAGGAAAACCTGGATCCCTTTAATGAGCACACGGGTGAGGAACCTGTGGAATCCCTTAC 259

Qy 3452 AAGAGGTACAACTTAAAGAACCACTTGAAGATCTTCTGGTAAATGGATCTCAATTAG 3511

Db 258 AAGAGGTACAACTTAAAGAACCACTTGAAGATCTTCTGGTAAATGGATCTCAATTAG 199

Qy 3512 CAGAAATCAGGATCCAAATTTTAGTGTGGACAAACCACTGTGTGCC 3559

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RESULT 15

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LOCUS BE838720 377 bp mRNA linear EST 22-SEP-2000

DEFINITION RC6-FN0112-190700-021-E06 FN0112 Homo sapiens cDNA, mRNA sequence.

ACCESSION BE838720

VERSION BE838720.1 GI:10271098

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 377)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matekuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=st2-RC6-FN0112-190700-021-E06&t3=2000-07-19&t4=1)  
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FEATURES

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ORIGIN

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Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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